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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   766.2
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BM693867 UI-E-DW1-
BM670929 UI-E-DW1-
                                                                               Description
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Verto
Mammalia; Eutheria; Primates; Catarrhini; Hoi
1 (bases 1 to 869)
1i, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
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/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week)"
/lab_host="DH10B"
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sapiens cDNA clone CS0DF016YG03 5
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A182649 wk57b12.x
A1627783 ty82a11.x
A1621783 ty82a11.x
A1911549 ty73d09.x
BE047352 hq79e01.x
BM030860 49538 MA
BG384365 303426 MA
BG384365 303426 MA
BF194822 7089a04.x
A1538624 tp75g12.x
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BF10326 7n5701.s
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AR57205 zj60f04.s
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AR287951 zs55b03.r
BF92154 MR1.WT017
AR287951 zs55b03.r
BF740045 yc42g04.x
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W61239 zd31d10.s1
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GTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCC
                                                                              TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTT
                                                                                                                                     ACTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACACCACTATCA 654
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                                                                                                                                                                                                                                                                                                                                              910;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NH_MGC Library."
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5182255"
/clone=lib="NIH_MGC_115"
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NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
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Pred. No. 2.1e-122;
0; Mismatches 33;
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908 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODF016YG03 3
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
1 (Aruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
TGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCTTGGTGGTGAAATG
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/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                         pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : http://fulllengch.invitrogen.com"
/organism="Homo sapiens"
/db_xref="teaxon:9606"
/clone="CSODFO16VG03"
/clone lib="LTI_FL013_FBrn1"
/dev_etage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
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                                                                                                                                                                                                                                                                                                  Length 908;
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                                                                                                                                                                                                                                                                                                  41.9%; Score 765.4; DB 9;
93.8%; Pred. No. 2.9e-122;
live 27; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                        225
                                                                                                                                                                                                                                                                                                                              Matches 841;
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
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520 AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGG
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ORGANISM
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BM693867
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 703)

S. Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Pu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

Homo sapiens cDNA ADC clones

Unpublished (2000)

Contact: Zeguang Han

Si Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Si Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-5080192

Email: hanag@chgc:sh.cn

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                         AV709899 ADC Homo sapiens cDNA clone ADCACB04 5', mRNA sequence.
AV709899
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="ADCAGD4"
/clone="ADCAGD4"
/tissue_type="Adcada gland"
/dev_stage="Adult"
/lab host="SOGR"
/lote="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                     1668
1549 CCTATCCCACCAATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 GCAACTICCAGICCIACAGCIGIGAGGIGCAATIACACAGAGGCCTICCAGACTCAGA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCAGACCCTCTGGTGGTAAATGGACATTTTCCTATATCGGCTTCCCTGTAGAGCTGAAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 CCAGACCCTCTGGTGGTAAATGGACATTTTCCTATATCGGCTTCCCTGTAGAGCTGAACA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 cagrerarrearregegececaraararrecraargeaarrargaargaagaregeceerr 180
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                                                                                                                                     1669 AATGTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATA 1725
                   177 CCTATCCCMCCAATTACAGGGMAAAAACGTGTGATGATCCTGAAGCTTACTATGCASCCT
                                                                   1609 ACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATATTACTAACT
                                                                                       117 ACAAACAGCCTTAGTAATTAAAACATTTTATAMHWATAAAATTTTCAAATATTGCTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
35.3%; Score 645.4; DB 10
Best Local Similarity 97.5%; Pred. No. 1.4e-101;
Matches 655; Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 t
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                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
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SOURCE
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JOURNAL
COMMENT
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Genome Res. 6 (9), 791-806 (1996)

The Genome Res. 6 (9), 791-806 (1996)

The Genome Fes. 6 (9), 791-806 (1996)

The Gontact: Soares, MB

The Contact: Soares, MB

The Contact Soares, Mayor Soares, Mayor Soares, Mayor Soares, Mayor Soares, MB

The Contact Soares, MB

The Contact Soares, Mayor Soares, Mayor Soares, Mayor Soares, MB

The Contact Soares, Mayor Soares,
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UI-E-DW1-ahe-i-22-0-UI.rl UI-E-DW1 Homo sapiens cDNA clone
UI-E-DW1-ahe-i-22-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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I (bases 1 to 652)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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241 AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGG
                                                                                                                                                                                                                   AGACAGTAGAAGTGAACTTCACAACCACCCCTGGGAAACAGATACATGGCTCTTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACACAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 CATAITITICCIACITGIGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCC
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                                                                                                                                                                                                                                                                                                                                                                             640 AACACCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACAGAAGAACAAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 GAGCTTCAGTGGTGATTCCAGTGACTGGGGGATAGTGAAGGTGCTACGGTGCTGCTGCTGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="UI-E-DW1-ahe-i-22-0-UI"
/clone lib="UI-E-DW1"
/tissue_type="lens"
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BM670929
BM670929.1
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/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EoR I; Site 2: Not I;
UI-E-DW1 is a normalized CDNA library containing the
following tissue(s): lens. The library was constructed
according to Bonaldo, Lennon and Soarse, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
strande cDNA was ligated to on EcoR I adaptor, digested
with Not I, and cloned directionally into pT713-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CGATTAGCGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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34.9%; Score 638.4; DB 14; Length 652;
Best Local Similarity 99.7%; Pred. No. 2.3e-100;
Matches 650; Conservative 0; Mismatches 1; Indels 1;
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BM670929/c
LOCUS
DEFINITION
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BM670929 G57 bp mRNA linear EST 27-FEB-2002 UI-E-DW1-ahe-i-22-0-UI.sl UI-E-DW1 Homo sapiens cDNA clone UI-E-DW1-ahe-i-22-0-UI 3', mRNA sequence.

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/dev stage="adult"
/lab_host="modified Technologies) (T1 phage resistant)
/lab_host="DH10B (Life Technologies) (T1 phage resistant)
/note="DG7gan: eye: Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DW1 is a normalized cDNA library containing the
following tissue(s): lens. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG LIB=UI-E-DMI
                                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 315 8250
Tel: 319 315 8250
Emai: 319 315 9562
Emai: smooares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Sequencing (www.resgen.com).
Seg primer: M13 Forward
POLYA-Yes.
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                           Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="UI-E-DW1-ahe-i-22-0-UI"
/clone lib="UI-E-DW1"
/tissue_type="lens"
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Pred. No. 5e-99;
0; Mismatches
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116 c 150 g
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GI:18980826
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ilarity 98.5%;
Conservative (
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Bonaldo, M.F., Lenno
                                                                                        Homo sapiens
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human.
Query Match
Best Local Simi
Matches 651;
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BE539514
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DEFINITION
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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1 (Dases 1 to 676)

2 (Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Pu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z.. and Han,Z.

Lino sapiens cDNA HTC clones

Lino sapiens cDNA HTC clones

Lino sapiens CDNA HTC clones

Longual Human Genome Center at Shanghai

231 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc:sh.cn

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AV727345 HTC Homo sapiens cDNA clone HTCACC09 5', mRNA sequence. AV727345 II:10836766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="HTC"
/tissue_type="Hypothalamus"
/dev stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
Xho1"
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                                                              GTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTTGTAGCCACCCCCCC
                                                                                                                                                CATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCAATTACAGGG-AAAAACGTG
                                                                                                                                                             CATGAGAAGCAAGAGCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTG
                                                                                                                                                                                                              237 TGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAAACATTTAT
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                                                                                               GTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACC
                       477 Greractriagagaringaracaaaagacgarracaargerereagrerereceaag
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db_xref="taxon:9606"
clone="HTCACC09"
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ACCESSION
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601060209F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446667 5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Satuatsberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                      GAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGT
                                                                                                                                                                                                                                                                               ATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCACAACCACTCCCCTG
                                                                                                                                                                                                                                                                                                                                                                      GGAAACAGATACATGGCTCTTATCCAACACACCACTATCATCGGGTTTTTCTCAGGTGTTT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Ammanla; Butheria; Primates; Catarrhini; Hominidae; Homo
I (Dassa I to 641)
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H
                                                 Indels
       Length
Score 628; DB 10;
Pred. No. 1.4e-98;
0; Mismatches 20;
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    34.4%;
ilarity 96.9%;
Conservative
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ACTCTTGAAAGG
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1275 CCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATAC 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1695 ACTACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 641;
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99.2%; Pred. No. 1.8e-97;
iive 0; Mismatches 4;
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                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:944667"
/clone lib="NIH MGC_10"
/cell line="MGG36"
/lab_host="DH108"
                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                            High quality sequence stop: 639.
Location/Qualifiers
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Best Local Similarity 99.2
Matches 635; Conservative
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos I Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Miklos I R.N.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1702 row: e column: 12
High quality sequence stop: 784.
                  BI458542 11-AUG-2001
603198643F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5278067 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /not="Organ: brain; Vector: pBluescriptR (modified pBluescript K8+); Site_1: BamH1; Site_2: Sall-KhoI (grog p: organized proper S'-TTTTTTTTTTTTTVN-3' size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATABATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGGAATTTCACC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629
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                                                                                                                                                                                                                                   1 (bases 1 to 788)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.4e-95;
0; Mismatches 2; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .788
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5278067"
/clone=lib="Wiff MGC 96"
/tissue_type="hypothalamus"
/lab_host="DH108"
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Best Local Similarity 98.9
Matches 656; Conservative
                                                             mRNA sequence.
                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EG433769 630 bp mRNA linear EST 14-MAR-2001
602497744F1 NIH_MGC_75 Homo gapiens cDNA clone IMAGE:4611491 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1358 row: g column: 12
High quality sequence stop: 610.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 630)

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428 TTTTCTCAGGTGTTTTGAGCCACACAGAAACAAACGCGGAGCTTCAGTGGTGATTCCA 487
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone="INAGE:4611491"
/clone lib="NIH MGC 75"
/lab_host="DH10B (TĪ phage-resistant)"
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/organism="Homo sapiens"
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BG433769
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BI602183.1 GI:15495122
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 842)
INH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs.~Gemail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninot (RIREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                TTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGC
                                                                                                                                                   626 TCCTTCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGCC
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Length 630;
  DB .12;
Score 598.2; DB.1.
Pred. No. 1.9e-93;
0; Mismatches 13
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32.7%;
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1444 TCCATGTCAAGCAGCAGCTGTCAGCAGGAAAAGATCACAAGCCTGCCACGATGGCTGCT 1503
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                                                                                                                                                                        /note="Organ: brain, Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (gtcga pluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (gtcga primer boligo-dT primed using primer 5. TTTTTTTTTTTVN-3, size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/WHGRI, Mational Institutes of Health). Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLANL24 row column: 02
High quality sequence stop: 807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 CATAATATCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCCCATTAAGGTTCTTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                             CATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACC
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                                                                                                                                                                                                                                                                                                                                         DB 13; Length 842;
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                                                                                                                                                                                                                                                                                                                                      Score 588; DB 13; 1
Pred. No. 1e-91;
0; Mismatches 25;
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                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone=!nhags:5286745"
/clone=lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_hogt="DH108"
                                                                                                                                                                                                                                                                                               205 g
                                                                                                                                                                                                                                                                                                                                      Query Match 32.2%;
Best Local Similarity 95.0%;
Matches 684; Conservative
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                                                                                 source
                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
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AW970151 680 bp mRNA linear EST 01-JUN-2000 EST382232 MAGE resequences, MAGK Homo sapiens CDNA, mRNA sequence. AW970151
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1017 TACCCATCTGAAATATGTTTCCATCACAATTTGTTACTTCACTGAATTTCTTCAAAAC 1076
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, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                          Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
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/db xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptsKm" 1 c
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122 ATCTAATCCCGGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAA 181
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AW299271/c
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AUTHORS
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KEYWORDS
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E. (Dases I to 561)

S. (Dases I to 561)

I. (Dases I to 561)

L. Onter Esta: bladee; of Health, Mammalian Gene Collection (MGC)

L. Onter Esta: bbadee6.x1

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cond through the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

image. 1101.gov/kinage/html/iresources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                         AW675096 561 bp mRNA linear EST 11-APR-2000 bb40e05.yl NIH MGC 12 Homo sapiens cDNA clone IMAGE:2985728 5' similar to TR:043844 043844 IL-17 RECEPTOR. ;, mRNA sequence.
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/db xref="tracm."
/db xref="tracm."
/clone="lMAGE:2985728"
/clone="lb="NIH MGC 12"
/tissue_type="cervical carcinoma cell line"
/lab_host="cervical carcinoma cell line"
/lab_host="cervical carcinoma cell line"
/loce="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Technologies."
                                                       1563
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                                                                            GCTCCTTGTAGCCCCACCATGAGAAGCAAGAACCTTAAAGGCTTCCTATCCCAACAATT
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ACAGGG-AAAAACGTGTGATGAT-CCTGAAGCTTACTATGCAGCCTACAAACAGCCTTA
                                                       GCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACTTAAAAGGCTTCCTATCCAACTT
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                                                                                                                                                                                                                            GTAATAAAA---CATTTTATCCAATAAAATTTCAAATTTTGCTTAACTA 646
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No. 7.4e-86;
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Pred. 1
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AW675096.1 GI:7540331
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Best Local Similarity 99.3%;
Matches 556; Conservative
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ORIGIN
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TITLE
JOURNAL
COMMENT
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW299271 510 bp mRNA linear EST 18-JAN-2000 xs48h02.x1 NCI_CGAP_Kidl1 Homo sapiens cDNA clone IMAGE:2772915 3',
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                                                           caggggactartcaartrigargaargraagcraggractccgggggagargccagcarcc
                                                                                                                                                                              GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAAT
                                                                                                                                                                                                                                                                                                                 302 GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCTCTGGTGGTAAAT
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
I (bases 1 to 51)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Primates, Catarrhini, Hominidae, Homo.
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/db xref="taxon:9606"
/clone="IMAGE:2772915"
/clone_lib="NVI_GGAP_Kid11"
/lab_host="DH10E"
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High quality sequence stop: 457.
Location/Qualifiers
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TGTGGGATCCGAACATCACT
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Homo sapiens cDNA clone IMAGE:3566736 3',
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP chone distribution information can be
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                       Length 510;
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                                                                                                                                     27.2%; Score 497; DB 10;
larity 99.0%; Pred. No. 5.3e-76;
Conservative 0; Mismatches 5;
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mRNA sequence.
                                                          Fatima Bonaldo.
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found through the I.M.A.G.E. Consortium/LINL, send email
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/organism="Homo sapiens"
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                                  info@image.llnl.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 470.
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Patent No. US2020102639A1

GENERAL INFORMATION:
APPLICANT: Shaughnessy, John D.
TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
FILE REFERENCE: D6138

CURRENT APPLICATION NUMBER: US/09/778,971

CURRENT FILING DATE: 2000-02-02

PRIOR APPLICATION NUMBER: US 60/180,374

PRIOR PILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9
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100.0%; Pred. No. 0;
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; OTHER INFORMATION: CDNA Of human Evi27
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Best Local Similarity 100.
Matches 1827; Conservative
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Compugen Ltd.
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US-09-874-503-11

US-10-000-157-11

US-10-003-547-157

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US-10-176-78-399

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Score

Result

	Oy 1501 GCTGCTCC            Db 1501 GCTGCTCCT   Qy 1561 ATTACAGG	1621 1621 1681 1681	OY 1801 AAAAAAAA  Db 1801 AAAAAAAA	RESULT 2 US-09-886-404-17 ; Sequence 17, App ; Patent No. US200 ; GENERAL INFORMAT ; APPLICANT: Medli	HAPLICANT: SILL HAPLICANT: BIN HAPLICANT: NGIN HAPLICANT: JING HILD OF INVENT HILL OF INVENT HILL OF INVENT HILL OF INVENT HILL REFERENCE: CURRENT FILING I	PRIOR APPLICATION PRIOR PILLING DAY PRIOR FILLING DAY SOPTWARE: PATENT	; SEQ ID NO 17 ; LENGTH: 1841 ; TYPE: DNA ; PEATURE: ; RAME/KRY: CDS ; LOCATION: (50). US-09-886-404-17	Query Match Best Local Simila Matches 1789; Cc Qy 1 CGCGATG1
241 GCTTGTTGAAGGCCACCAAGATTTGTGACGGCAAAAGCAACTTCCAGTCCTACAGCT 300 241 GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGCAAAAGCAACTTCCAGTCCTACAGCT 300 301 GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACCACACACCTCCAGTGGTAAAT 360 301 GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACCAGAC	421 ATANTATTCCTAATGCAAATATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCT 480		661 TTTCTCAGGTGTTTGAGCCACACCAGAACAACGCGAGCTTCAGTGGTGATTCCAG 720 [	781 GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCC 840	901 TGGTGGCCACATGGGTGGTGGCAGGATCTATCTAATGTGGAGGCACGAAAGGATCA 960	1021 CATCTGAAATATGTTTCCATCACAATTTGTTACTTCACTGAATTTCTTCAAAACCATT 1080	1141 TGCAGTGGCTTGCCACACAAAGAAGGCAGCAGAAAGTCGTCTTCCTTC	1261 CTCAAGACCTCTTCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTC 1320
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Jing, Shugtan

ENTION: II-17 Like Molecules and Uses Thereof

MCE: 01017/31288

LICATION NUMBER: US/09/886,404

ING DATE: 2001-06-21

SATION NUMBER: 09/810,384

SATION NUMBER: 60/266,159

SATION NUMBER: 60/266,159

SATION NUMBER: 60/213,125

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SQID NOS: 22
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45 CGGCGATGTCGTCTGTGCTGCTGCTGCCGCGCTGTGCAGGACGCCCTACCCCGAG 104 61 AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCGCTCTCCAGAGTGGCTGCTACCAGAGTGGATGTACAAAGTGTGCTACAAGTTGTGTTCTGAAACTTGGGCCATCTCCAGAGTGGATGCTACAAAGTGTGCTTCTAAAGTGGGCCATCTCCAGAGTGGATGCTACAAAGTGTTGCAA 180		241 GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT 300 	301 GTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCAGACCTCTGGTGGTAAAT 360 	361 GGACATTTCCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTCATTGGGGCCC 420 	421 ATAATATTCCTAATGCAAATATGAAGAATGGCCCTTCCATGTCTGTGAATTTCACCT 480 	481 CACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCC 540 	541 IGIGGGAICCGAACAICACIGCTIGITAAGAAGAATGAGGAGACAGIAGAAGIGAACTICA 600 	601 CAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGT 660 	661 TITCTCAGGTGTTTGAGCCACACAGAAGAACAACGCGAGCTTCAGTGGTGATTCCAG 720 	721 IGACTGGGGAIAGTGAAGGTGCTACGGTGAGCTGACTCCATATTTCCTACTTGTGGCA 780 	781 GCGACTGCATCATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCC 840 	841 CTCTGGATAACAACAAAGCAGGCGGGAGGCTGGCTGCCTCCCTC	901 TGGTGGCCACATGGGTGCTGGTGGATCTATCTAATGTGGAGGACGAAGGATCA 960 	961 AGAAGACTICCTITICIACCACCACACIACTGCCCCCCATIAAGGITCIIGIGGITIACC 1020 1005 AGAAGACTICCITITCIACCACCACACIACTGCCCCCCATIAAGGITCIIGIGGITIACC 1064	1021 CATCTGAAATAIGITTCCATCACACAATTIGITACTTCACTGAATTTCTTCAAAACCATT 1080 	1081 GCAGAAGTGAGGTCATCCTTGAAAGTGGCAGAAAAGAAA
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man, Daniel M.
TION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
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TATION NUMBER: US/09/863,818A
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APPLICANT: Yeh, Richard
APPLICANT: Yeh, Richard
APPLICANT: Silbiger, Scott M.
APPLICANT: Bliot, Gary S.
APPLICANT: Nguyen, Hung Q.
APPLICANT: Nguyen, Hung Q.
APPLICANT: Jing, Shuqian
TITLE OF INVENTION: IL-17 Like Molecules and Use
FILE REPERENCE: 01017/37128
CURRENT APPLICATION NUMBER: US/09/886,404
CURRENT APPLICATION NUMBER: 09/810,384
PRIOR APPLICATION NUMBER: 09/810,384
PRIOR APPLICATION NUMBER: 60/266,159
PRIOR PRING DATE: 2001-02-02
PRIOR PRING DATE: 2001-02-02 RESULT 4
US-09-886-404-19
IS-09-886-404-19

, Sequence 19, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:

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Best Local Similarity 89.3%;
Matches 1758; Conservative
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 2015
TYPE: DNA
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                    PRIOR APPLICATION NUMBER: US PCT/USO0/34956
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-11-10
PRIOR PELING DATE: 2000-11-10
PRIOR PELING DATE: 2000-08-24
PRIOR PELING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-02
PRIOR PLING DATE: 2000-08-02
PRIOR PLING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/USO0/0541
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/USO9/31274
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-01
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Best Local Similarity 99.8
Matches 1511; Conservative
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SEQ ID NO 11
LENGTH: 1515
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; ORGANISM: Homo Sapien
US-09-874-503-11
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1965 TAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTC 2012
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APPLICATION NUMBER: US PCT/US01/06520
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PRIOR APPLICATION NUMBER: US 60/243,646

PRIOR FILING DATE: 2000-11-28

PRIOR PELING DATE: 2000-11-26

PRIOR PELING DATE: 2000-10-26

PRIOR PELING DATE: 2000-10-26

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PRIOR PELING DATE: 2000-10-11

PRIOR PELING DATE: 2000-01-11

PRIOR PELING DATE: 2000-01-11

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PRIOR PELING DATE: 2000-01-11

PRIOR PELING DATE: 2000-01-21

PRIOR PELING DATE: 2000-06-22

PRIOR PELING DATE: 1999-06-09

PRIOR PELING DATE: 1999-06-09

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-04-21

PRIOR PELING DATE: 2001-05-10

PRIOR PELING DATE: 2001-05-20

PRIOR PELING DATE: 2000-08-25

PRIOR PELING DATE: 2000-08-25
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CURRENT FILING DATE: 2001-06-05
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Gurney, Austin L.
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Hymowitz, Sarah G.
Tumas, Daniel
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Wood, William I.
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Filvaroff, Ellen
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GENERAL INFORMATION:

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Pred. No. 0;
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PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR PLING DATE: 1999-03-08
PRIOR PLING DATE: 1999-03-08
PRIOR PLING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR PLING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/05611
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR PLING DATE: 2000-06-02
PRIOR PLING DATE: 2000-06-02
PRIOR PLING DATE: 2000-06-02
PRIOR PLING DATE: 2000-11-10
PRIOR PLING DATE: 2000-11-10
PRIOR PLING DATE: 2000-12-01
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-06-09
PRIOR PLING DATE: 2001-06-20
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PRIOR PLING DATE: 2001-06-20
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Best Local Similarity 99.8%;
Matches 1511; Conservative
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US-09-747-259-11
Sequence 11, Application US/09747259
Publication No. US20030008815A1
GENERAL INFORMATION:
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APPLICANT: Eaton, Dan L.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230RCI
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
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                                                                                                                    ; Sequence 157, Application US/10063547; Publication No. US20020182638A1; GENERAL INFORMATION:
                 GCTGCTCCTTGTAG 1515
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; ORGANISM: Homo Sapien
US-10-063-547-157
   GCTGCTCCTTGTAG
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APPLICANT: Yangura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF FILE REFERENCE: P1381R1C1P1(US)
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Pred. No. 0;
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CURRENT FILING DATE: 2000-12-20
PRIOR PEPLICATION NUMBER: US/09/311,832
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/USO0/04341
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR APPLICATION NUMBER: PCT/USO0/0532
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-10
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Williams, P. Mickey
Wood, William
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Hillan,Kenneth
Tumas,Daniel
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Filvaroff, Ellen
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Best Local Similarity 99.8
Matches 1511; Conservative
                                                                                                           Godowski, Paul
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ORGANISM: Homo Sapien
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Goddward, Paul J.
APPLICANT: Granth, Yuctoria
APPLICANT: Matanaba, Colin K.
APPLICANT: Watanaba, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PAJORIC42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT APPLICATION NUMBER: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
INDIGHTHE OF SEQ ID NOS: 612
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99.8%; Pred. No. 0;
iive 0; Mismatches
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Publication No. US20030008352A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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Matches 1511; Conservative
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CORGANISM: Homo Sapien
US-10-174-590-399
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US-10-174-590-399
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Db 362 GGACATTTCCTACATCGGCTTCCCTGTAGA	Oy 421 ATAATATTCCTAATGCAAATATGAATGAAGA 	Qy 481 CACCAGGCTGCCTAGACCACATAATGAAATA	Qy 541 TGTGGGATCCGAACATCACTGCTTGTAAGAA 	OY 601 CAACCACTCCCTGGGAAACAGATACATGGC	Oy 661 TTTCTCAGGTGTTTGAGCCACACCAGAAGAA  Db 662 TTTCTCAGGTGTTTGAGCCACACCAGAAGAA	Qy 721 TGACTGGGGATAGTGAAGGTGCTACGGTGCA 	Qy 781 GCGACTGCATCCGACATAAAGGAACAGTTGT 	Qy 841 CTCTGGATAACAAAAGCAAGCCGGGAGG	Oy 901 TGGTGGCCACATGGGTGCTGGTGGCAGGAT	Oy 961 AGAGACTTCCTTTTCTACCACCACACTACT	Oy 1021 CATCTGAAATATGTTTCCATCACACAATTG	Qy 1081 GCAGAAGTGAGGTCATCCTTGAAAAGTGGCA 	Oy 1141 TGCAGTGGCTTGCCACTCAAAGAAGGCAGC Db 1142 TGCAGTGGCTTGCCACTCAAAAGAAGGCAGC	Qy 1201 ACGTCAACAGTGTGTGCGATGGTACCTGTGG 	Oy 1261 CTCAAGACCTCTTCCCCCTTGCCTTTAACCT	Qy 1321 ATCTGCACAAATACGTGGTGGTCTACTTTAG	Qy 1381 CTCTCAGTGTCTGCCCCAAGTACCACTTCAT	Oy 1441 TTCTCCATGTCAAGCAGCAGGTGTCAGCAGG
1322 ATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATG	1381 CTCTCAGTGTCTGCCCCAAGTACCACTTCATGAAGGATGCCACTGCTTTTGTGGAGAAC  1382 CTCTCAGTGTTGCCCCCAAGTACCACCTTGTTGAAGGATGCCACTGCTTTTTTTT	1442 TTCTCCATGTCAAGCAGC	Oy 1501 GCTGCTCCTTGTAG 1514  Db 1502 GCTGCTCCTTGTAG 1515	RESULT 10 US-10-176-758-399 ; Sequence 399, Application US/10176758	Publication GENERAL INFO APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:			CURRENT APPLICATION NUMBER: US/10/176,758 ; CURRENT FILING DATE: 2002-06-21 ; Prior Application removed - See File Wrapper or Palm ; NUMBER OF SEQ ID NOS: 612		Othery Match  Query Match  Query Match  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	COTGCTGATAAGCCTGGCGGCTGTGCAGGAGCGCCGTACCCCGAG 60	61 AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACACATG	121 AICTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAA 122 AICTAATCCCCGGAGACTTGAGGGACCTCCGGAGTAGAACCTGTTACAACTAGTGTTTGCAA 122 AICTAATCCCCGGAGGAGTAACTAGAGGACTACGAACTTAGTAGTGTTAGTAACTAGTGTTAGTAACTAGTGTTAGTAACTAGTGTTAGTAACTAGTGTTAGTAACTAGTGTTAGTAGTGTTAGTAGTGTTAGTAGTGTTAGTAGT	181 CAGGGACTATTCAATTTGATGAATGTAAGGTGGGTACTCGGGCAGATGCCAGCATC 182 CAGGGGACTATTCAATTTGATGAATGTAAGGTGGGTACTCCGGGCAGATGCCAGCATC 183 CAGGGGACTATTCAATTTGATGAATGTAAGGTACTAGGCAATGCCAGCAATGCAAAGGTAATGTAATGAATG	241 GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT	301 GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCGACC	361 GGACATTTCCTATATCGGCTTCCCTGTAGAGCTGAACAGACTGTTTTTTTT

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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF DATE: 2002-05-03
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEG ID NO 157
TENCHUL A.
 1442 TTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCT 1501
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82.6%; Score 1509.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches
                                                                                                                                             ; Sequence 157, Application US/10063616; Publication No. US20030013855A1; GENERAL INFORMATION:
                                                                                                                                                                                                            Filvaroff, Ellen
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                             APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, E
APPLICANT: Gerritsen, M
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ORGANISM: Homo Sapien
                                   GCTGCTCCTTGTAG
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US-10-063-616-157
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                       TITCICAGGIGITITGAGCCACACCAGAAGAAACAAACGCGAGCTICAGTGGTGATTCCAG
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US-10-063-502-157
; Sequence 157, Application US/10063502
; Publication No. US20030023042A1
; GENERAL INFORMATION:
    APPLICANT: Eaton, Dan L.
; APPLICANT: Gerriteen, Mary E.
    APPLICANT: Gedrard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
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                                                                       APPLICANT: Cancer, Jucc.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Ran, James
APPLICANT: Ran, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLI
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Publication No. US20030013153A1
                   GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399
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APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/063, 502
CURRENT PILING DATE: 2002-0.5-0.1
Prior Application removed - See File Wrapper or Palm
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99.8%; Pred. No. 0;
iive 0; Mismatches
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Best Local Similarity 99.8
Matches 1511; Conservative
                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-502-157
                                                                                                          SEQ ID NO 157
LENGTH: 1515
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Garney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 399
LENGTH: 1515
                                           ; TYPE: DNA
; ORGANISM: Homo Sapien
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
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APPLICANT: Wacanabe, Colin K.
APPLICANT: Wacanabe, Colin K.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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FILE REFERENCE: P3430R1C5
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NUMBER OF SEQ ID NOS: 612
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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CORGANISM: Homo Sapien
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       US-09-257-825B-10
US-08-628-417-6
US-07-861-458C-4
US-08-747-221B-24
US-08-747-221B-26
US-09-005-051-26
US-09-005-051-26
US-09-014-969-11
US-09-247-373B-25
US-09-247-373B-25
US-09-247-373B-25
US-09-247-373B-25
US-09-247-373B-25
US-09-247-373B-25
US-09-257-359-13
US-09-661-800-1
US-09-661-569-1
US-09-661-569-1
US-09-661-569-1
US-09-227-357-139
PCT-US92-06300-1
US-09-385-982-262
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Sequence 2, Appli Sequence 4, Appli	Sequence 8, Appli Sequence 1, Appli		Sequence 4, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 7, Appli	Sequence 13, Appl	Sequence 8, Appli	Sequence 59, Appl	Sequence 31, Appl	Sequence 12, Appl

## ALIGNMENTS

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US-09-056-075-1
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US-09-056-075-1
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Sequence 1, Appr---
No. 5955368
                                                                                                                                                                                 TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
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APPLICANT: Johnso
                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                          MOLECULE TYPE: FEATURE:
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APPLICANT: Rood, Jul:
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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             NAME/KEY: misc feature LOCATION: 3770..4013
OTHER INFORMATION: /not
OTHER INFORMATION: plas
                                                                                                        STRANDEDNESS:
TOPOLOGY: li
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STATE: WI
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                                                                                                                                     TYPE:
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                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                    ENGTH:
                                                                                                                     nucleic acid
EDNESS: double
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                                                                                                                                                6243 base pairs
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plasmid RP4"
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Best Local Similarity

2.9%;

Score 53; DB 2; Pred. No. 0.00055;

Length 6243;

Query Match

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Query Match
Best Local :
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                                                                                                                                                                             TELEFAX: (619) 235-0176
[NFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      itent No.
                                                              MOLECULE NO
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1358 АЛАЛАЛАТАЛАЛАЛАТАТАЛАЛАТАЛАЛАЛАТАЛАЛА 1394
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                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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 Local Similarity
                                                                                                                          STRANDEDNESS:
                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                             NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 10-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATCAATTACAGCTTTAATTGAAAAACTGTAACCATTTTGATAATGCAACAATAAAGCAT 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  АБАЛАВАТАЛАВАЛАТАЛАВАВАТАЛАВАВАЛАВАТАЛАВАВАТАЛАВАТАЛАВАТАЛАВ 1297
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                                                                                                                                                              19124 base pairs
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Miller, Louis H.
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                Length 19124;
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US-08-655-352-10
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                                                                                                                                                                                                                    TELEPHONE: (503) 226-73
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15635
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 08/323,449
APPLICATION NUMBER: 08/323,449
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                                                                   FEATURE
                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                                                                                                     FILING DATE: October 14, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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            NAME/KEY:
NAME/KEY:
LOCATION:
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                                                                                                                             TYPE:
STRANDEDNESS: GOU
                                                                                   DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One World Trade Center STREET: 121 S.W. Salmon Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                            NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ТТАТАЛАЛАЛАЛАТАЛАЛАСЛАЛАСБАЛБАЛАЛАЛАЛА 15672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAATCAATTACAGCTTTAATTGAAAAACTGTAACCATTTTGATAATGCAACAATAAAGC 1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shameekumar Patil, Daisuke Takezawa
VENTION: COMPOSITIONS AND METHODS FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WordPerfect 5.1
              protein-coding sequence (not including
stop codon)
nucleotides 20-1570
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                                                                                 sequence
                                                                                                 CDNA to mRNA
Tobacco CCaMK cDNA and
                                                                                                                                                    double stranded
                                                                                                                                                                                                                                                       226-7391
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                                                                                                   amino-acid
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (503) 228-94.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                        NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1668
                                                            1719
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1668 TTTTATCACTACTCGTAAAAAGATCCTTTAAATTAATTCGGAAGCCTTTATGGTAAAAAA 1727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                         OLECULE TYPE:
                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Portland
                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                            DESCRIPTION:
                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                 STRANDEDNESS: double stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klarquist Sparkman Campbell Leigh
                                                                                                                                                                                                                                           DESCRIPTION:
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                             TTTTATCACTACTCGTAAAAAGATCCTTTAAATTAATTCGGAAGCCTTTATGGTAAAAAA 1727
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6362395
                                                         TTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCA 1778
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                                                                                         Conservative
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                                                                                                                                                                nucleotides 20-1570
                                                                                                                                                                                           protein-coding sequence
                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                stop codon)
                                                                                                                                                                                                                            sequence
                                                                                                                                                                                                                                       cDNA to mRNA
Tobacco CCaMK cDNA and deduced amino-acid
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                                                                                       Score 49.8; D
Pred. No. 0.00
0; Mismatches
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Pred. No. 0.0021;
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                                                                                                                   DB 4;
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                                                                                                                   Length 1776;
                                                                                         Indels
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CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
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TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Poovaiah, APPLICANT: Patil, S
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TYPE: DNA
ORGANISM: Nicotiana tabacum
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTMAND: DESTRUCTION OF THE PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
              REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABERDEEN PROVING GROUND
                                                                                                                     FILING DATE:
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       ZIP: 21010-5423
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                                                       BIFFONI, ULYSSES J
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                                                                                                                                                                                                                                                                                                                             MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GILLESPIE, DAVID
VENTION: COMPETITOR PRIMER ASYMMETRIC
VENTION: POLYMERASE CHAIN REACTION
EQUENCES: 7
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US-08-628-417-6
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Best Local Similarity
Matches 113; Conserv
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                                              NFORMATION FOR SEQ ID NO:
                                                                                               NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
              SEQUENCE CHARACTERISTICS:
LENGTH: 1100
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IEM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1609 ACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATATTACTAACT 1668
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marchionni, Mark Andrew APPLICANT: Johnson, Carl D. TITLE OF INVENTION: HOMOLOGY CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
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                                                                    TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 04/01/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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nucleic acid
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51.6%;
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                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
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1743 GCTTTAATTGAAAATTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAAA 1802
                                                   2688 TATGGATTAATGTCAACATGTAAAATACAAATGCGGTTGTTAAAAATAATCTGTATTAAA 2747
                                                                                  1683 TAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACA 1742
                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotid
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
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ITTLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado Colnamby.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Verser, Carol Talk REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                              STRANDEDNESS: si
TOPOLOGY: linear
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nes 63; Conserv
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                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                    Score 49; DB 3;
Pred. No. 0.0042;
0; Mismatches 6
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Pred. No. 0.0025;
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                                                                                                                                                      Length 2836;
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                                                                                RESULT 10
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             Sequence 24, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                              1743 GCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAAA 1802
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
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APPLICANT: Wisnewski,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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6063610
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Silver, Gary W.
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ki, Nancy
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6063610ember 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37,459
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                          Sequence 26, Application US/09005051 Patent No. 6291222
                                                                                                                                        Patent No. 6291222
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: No. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
NAME: Verser Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
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TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
TUMBER OF SEQUENCES: 66
                                                                 APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nanc TITLE OF INVENTION: No. 62
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                  NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                     2748
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STATE: Colorado
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
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 ADDRESSEE:
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                   ADDRESSEE:
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llarity 58.6%;
Conservative
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Heska Corporation
                   Carol
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                   Talkington Verser, Ph.D
                                                                     No. 6291222el Carboxylesterase Nucleic Acid Molecules, Proteins and Uses Thereof
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Pred. No. 0.0042;
0; Mismatches 6
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US-08-242-677-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
Apple & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1803 АЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1743 GCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAA 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1683 TAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACA 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/747,221 FILING DATE: No. 6291222ember 12, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT FOR WINDOWS,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                               APPLICANT: Gaynor, Richard B
                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 TATGGATTAATGTCAÄCÄTGTÄAÄÄATACAÄÄTGCGGTTGTTAAAAATAATCTGTATTAAÄ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                        COUNTRY: US.
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                             CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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CLASSIFICATION:
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                                                                                                                                                                    P.O. Box 4433
                                                                                                           USA
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                         Cellular Nucleic Acid Binding Protein and Uses Thereof in regulating Gene E
                                                                                                                                                                                                                                           Treatment of AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version 7.0
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US-09-014-969-14
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Sequence 10, 5965397
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Best Local Similarity 69.1%;
Matches 67; Conservative
APPLICATION NUMBER: US/09/014
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1791 СТТССАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1731 AAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCAT 1790
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
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LOCATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge
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87 CambridgePark Drive
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Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
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Agostino, Michael J.
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                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO:

14:

SEQUENCE CHARACTERISTICS:

ENGTH:

2447 base pairs

STRANDEDNESS:

nucleic acid DEDNESS: double

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atent No. 6063570
GENERAL INFORMATION:
                                                                        TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1774
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MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                      TELEPHONE: 302-892-8112
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL.
                                                                                                                                                                                                                                                                         MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCGUNIUM, APPLICANT: O'KEEFE, DANIEL
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                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                        LENGTH: 991 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1007 MAKE
                              STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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6063570
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Pred. No. 0.0056;
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                                                                                                            Query Match
Best Local Similarity
Marches 65; Conserve
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                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: SOYBEAN
US-09-247-373B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-247-373B-25
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Best Local Similarity
Thes 65; Conserve
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                                                                                                                                                                                                                                         SOFTWARE: Mi
SEQ ID NO 25
LENGTH: 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09247373B Patent No. 6168954
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
                                                                                             1735 CAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTC 1794
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                               1795 САЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1827
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Pred. No. 0.0043;
0; Mismatches 28;
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Search completed: May 28, Job time : 165.735 secs 2003, 10:19:18

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11139.370 Million cell updates/sec
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## ALIGNMENTS

Human interleukin-17 receptor related protein (Evi27) encoding cDNA #1.

06-NOV-2001 (first entry)

AAD13443;

AAD13443 standard; cDNA; 1827 BP

RESULT 1 AAD13443

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Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21; Evi27; retroviral integration; chromosomal mapping; mutational analysis BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy; haematopoietic cell; cancer; autoimmune disease; ss. 02-FEB-2001; 2001WO-US03518. mat\_peptide CDS 09-AUG-2001. WO200157202-A2 sig\_peptide Homo sapiens. /\*tag= b 45..1511 /product= 6..1514 /\*tag= Location/Qualifiers product= \*tag= "Human Evi27 protein" "Human mature Evi27 protein" l analysis;
therapy;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a cDNA encoding human interleukin (II)-17 creceptor related protein (Bvi27). Human Evi27 gene was mapped to chromosome 3p21. Evi27 is a common site of retroviral integration in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful as antisense molecules to inhibit Evi27 protein or for chromosomal compaping or mutational analysis of Evi27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of Evi27 at the RNA or protein level is used in the treatment of diseases such as cancer corautoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1827; Best Local Similarity 100.0%; Pred. No. 0; Matches 1827; Conservative 0; Mismatches
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TGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCA
                                                                                    ATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCT
                                                                                                                                                                                                     ATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCT 480
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1560 1560	GCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCA	1501	Qy db
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1440 1440	ACCACTTCA:           ACCACTTCA:	1381 1381	D
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e e	GTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGJ 		od VQ
20	TGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTC	1141	Db
1140	CAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAAGAAAAATAGCAGAGATGGGTC CAGAGTGGCTTGCCACTCAAAAAGAAAGGAGAGACAAAAGTCGTCTTCCTTTCCTTTCCAA	1081	9 B
1140	GCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAAGAAAATAGCAGAGATGGGTCCAG	1081	δδ
1080	CATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATT	1021	pb Qy
1020 1020	AGAAGACTTCCTTTCTACCACCACACTACTGCCCCCCATTAAGGTTCTTGTGGTTTACC	961 961	gg Qg
960	TGGTGGCCACATGGGTGCTGGTGGCAGGATCTATCTAATGTGGAGGCACGAAAGGATCA	901	9d V2
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780	TGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCA	721	Q.
720	TTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAG	661 661	do VQ
660	CAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACACAC	601	D 09
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02-FEB-2001;
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  The invention relates to nucleic (IL-17)-like polypeptides. IL-17
                                                                                 Disclosure; Page 230-232;
                                                                                                                                                          Nucleic acid molecules encoding Interleukin 17 (IL-17) polypeptides useful in the treatment, prevention and d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of II-17 protein in an animal. The II-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction (rheumatoid arthritis, osteoarthritis, inflammatory joint disease); autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft vs. host disease); infections (HIV, (hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma leukaemia); reproductive (inflammation. The present sequence is human Interleukin-17 receptor B-2
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The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. asthma), skin disorders (e.g. aczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. sischaemia), eye disorders, reproductive disorders, tumours and
                                                                                                                                                                                                                                                                                                                                                     Jing
                                                                                                                                                                                                                               Three human nucleic acids encoding interleukin 17 (IL-17) receptor polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy: interleukin 17; immune system disorder; infection; weight; reproductive neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye
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12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0723232.
02-FEB-2001; 2001US-266159P.
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                                                                                                                                                                                                                                    Human; DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; gene therapy; protein therapy; immunological disorder.
                                                                                                                                                                                                                                                                      Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA
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P-PSDB; AAU11351.

Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -

Disclosure; Page 7-10; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents cDNA encoding the human DCRSS polypeptide.

Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;

Query Match Best Local Similarity

97.7%;

Score 1785.6; Pred. No. 0;

DB

24;

Length 1796;

В Ś 뮍 Ş 밁 5 Ś 밁 5 Ş 밁 Ş Ş 뮍 밁 망 Ś В á 밁 á 밁 Ş Matches 1788; 663 601 603 541 543 481 483 421 423 361 363 301 303 241 243 181 121 183 123 61 63 w GCGATGTCGCTCGTGCTGATAAGCCTGGCCGCGCTGTGCAGGAGGCGCCGTACCCCCGAGAG TGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCACA 602 CCAGGCTGCCTAGACCACATAATGAAATATATAAAAAAAGTGTGTCTAAGGCCGGAAGCCTG AATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCA TCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTG ACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTT TGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCACA CCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTG AATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCA ACATTTTCCTATATCGGCTTCCCTGTAGAGCTGAACAGTCTATTTCATTGGGGCCCAT ACATTTTCCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCCAT GTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGG GTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGG TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGT TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGT 302 GGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGC GGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGC 242 CTAATCCCGGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACA CTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACA 182 CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGAT 122 GCGATGTCGCTCGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGAT 120 Conservative 0; Mismatches 4; Indels 0; Gaps 542 422 362 180 662 482 660 600 540 480 420 360 300 240 60 62 0

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GTGGCCACATGGGTGCTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAG 960		
GCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAA		
CTGGATAACAACAAAAGCCAGGCAGGCTGCCTGCCTCCTCCTCCTCCTCCTCCTGCTGCTGCTG		
ATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTC		
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CTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCA		
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess foreign conversity, and for nutritional purposes. The present sequence is a cDNA biodiversity and for nutritional purposes.
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  CTCAAGACCTCTTCCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTC
                                                                             ACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACT
                                                                                                    ACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCCAGTGAGAACT
                                                                                                                                                           TGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTTCCCAATG
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                                                                                                                                                                                                                                                                                                                              Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
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                                                                                                                                                                                                                                                         Huntington's disease; Alzheimer's disease; chemotactic; chemo
haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
contraceptive; antiinfertility; antiinflammatory; ss.
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71..1531
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26..70
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26..1534
                                                                                                                                        /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
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GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT

CAGGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC

CAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC

ATCTAATCCCCGGAGACTTGAGGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAA

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AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG CGGCGATGTCGCTCGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAG

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Local Similarity

97.6%;

Score 1782.8; Pred. No. 0; Mismatches

DB 22; Length 1818;

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The present sequence is human protein with hydrophobic domain encoding CC cDNA clone HP10758. The polynucleotide and polypeptide of the invention CC may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The CC polynucleotides and its complementary sequences may also be used as DNA CC probes in diagnostic assays and also used in gene therapy. The CC polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and CC activity. The polypeptides and nucleic acids may be used as nutritional consultate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, complements to madulate the manufacturity and insulin-dependent diabetes), to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
Sequence 1818 BP;
                                                                       haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease). To modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kato
                                     modulate haemostatic and thrombolytic activity, to ligand activity, to modulate inflammation and to in
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The present sequence encodes a human interleukin 17-receptor-like protein (ILITRLP) variant. The ILITRLP polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to

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RESULT 8
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09-AUG-2000 cDNA encoding

interleukin 17-like receptor protein

Interleukin-17-like

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receptor;

(IL17RLP)-2.

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controlled in (IL-17RLP). IL-17RLP is a homologue of the II-17 receptor and has

a wide range of cytokine receptor-like activities. IL-17RLP or its

consists may be used to enhance host defenses against resistant chronic

and acute infections, e.g. mycobacterial infections, via the attraction

and activation of microbicidal leukocytes. It may also be used to

increase T-cell proliferation by stimulating IL-2 biosynthesis, for the

treatment of T-cell mediated autoimmune diseases and lymphocytic

treat sepsis. IL-17RLP may also be used to regulate hematopoiesis and to

treat sepsis. Extracellular IL-17RLP domains may be used as antagonists

of IL-17RLP. IL-17RLP agonists and antagonists can also be used to

modulate IL-6 expression, useful in treatment of cancers such as

myelomas, plasmacytomas and hybridomas and Lennert's Lymphoma. The

present cDNA sequence encodes human II-17RLP. This cDNA sequence was

derived from sequencing the HAPORAO cDNA clone (ATCC deposit
                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                        Matches 1800;
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16-SEP-1998;
16-MAR-1999;
                                                                                                                                                                                                                                                                                                                             Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides encoding interleukin-17-like receptor protein, useful for diagnosis and treatment of immune system-related disorders,
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 GGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGC 242
                                       CTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACA
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                                                                                                                                        CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCCAGAGTGGATGCTACAACATGAT 122
                                                                                                                                                                                 GCGATGTCGCTCGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG 167
                                                               CTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1816 BP;
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16-SEP-1998;
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The patent relates to novel interleukin-17-like receptor protein (IL-17RLP). IL-17RLP is a homologue of the IL-17
                                                  Novel polynucleotides encoding interleukin-17-like receptor useful for diagnosis and treatment of immune system-related e.g. sepsis and cancers -
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                                                                                                                                              GENOME
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98WO-US19121.
99US-0268311.
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peptide as described on Page 3
                                                                                                                                                                                                                                                                                            product= "Mature IL17RLP"
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Best Local Similarity
Matches 1795; Conserv
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1743 GCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAAA 1802 	B 8
1683 TAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACA 1742 	D Q
1623 TAATTAAAACATTTTATACCAATAAAATTTTCAAATATTACTAACTAATGTAGCATTAAC 1682 	B 8
1563 TACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAG 1622	B 성
503 TGCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAAT 15	g S
1443 CTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGC 1502 	g 8
1383 CTCAGTGTCTGCCCCAAGTACCACTTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTT 1442	B 64
1323 CTGCACAAATACGTGGTGGTCTACTTTAGAGAGAGTTGATACAAAAGACGATTACAATGCT 1382 	D 8
1263 CAAGACCTCTTCCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT 1322.	D Q
1203 GTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCT 1262	D 99
1143 CAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTTCCAATGAC 1202 	D D D
1083 AGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTG 1142 	Db Qy
1023 TCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGC 1082 	B 8
963 AAGACTTCCTTTTCTACCACCACACTACTGCCCCCCATTAAGGTTCTTGTGGTTTACCCA 1022	Db Qy
903 GTGGCCACATGGGTGGTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAG 962 	D Q
843 CTGGATAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTG 902	d d
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                                                                     The present sequence encodes human interleukin 17 receptor like protein (II17RLP), isolated from a cDNA library of human adult pulmonary tissue. II17RLP and its agonists can be used to treat disorders relating to cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration and ovulation, and neurogenesis. They can also be used to enhance host defences against resistant chronic and acute infections, e.g. mycobacterial infections via the attraction and acute cativation of microbial leukocytes. IL17RLP may also be used to increase T-cell proliferation by the stimulation of IL-2 biosynthesis for the treatment of T-cell mediated autoimmune diseases and lymphocytic differentiation of various haematopoietic progenitor cells, e.g. to cellase mature leukocytes from the bone marrow following chemotherapy, i.e. in stem cell mobilisation or to treat sepsis. The products can also be used for the diagnosis or treatment of immune system related disorders e.g. tumours, cancers, interstitial lung disease, and any disregulation of immune cell function including autoimmunity, arthritis, leukaemias, lowell disease or myell suppression, immunity, humoral immunity, inflammatory
  Sequence 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; interleukin 17 receptor like protein;
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  532 A;
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C; 399 G; 445
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Query Match Best Local

Similarity

97.2**%**; 99.1**%**;

Score 1775.2; Pred. No. 0;

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Length 1816;

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         Human; interleukin-17 receptor B-3; IL-17RB-3; immune system dysfunction; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obssity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alrheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; epilepsy; atherosclerosis; heart failure; angiogenesis; inflammation.
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                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1758; Conserv
                                                                                                                                                                                                                                Sequence 2015 BP;
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16-MAR-2001; 2001US-0810384
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Location/Qualifiers 50..1732 /\*tag= a /product= "Human IL-IL-17 receptor-like protein

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Best Local S
Matches 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obseity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischaemia), eye disorders, reproductive disorders, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Three human nucleic acids encoding polypeptides, useful for treating, preventing immune system disorders infections (e.g. viral infections)
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12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0723232.
02-FEB-2001; 2001US-266159P.
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                                                   Claim 1; Page
                                                                                                                                Polynucleotides and polypeptides encoding peptides, useful in diagnostic, forensic,
                                                                                                                                                                                                                                                                                                  Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1998;
25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome mapping; cancer; autoimmune disease; cardiovascular disord cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; forensic
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DB; AAB25795.
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identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                                       storing the sequence data on a computer system, and a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted proteins. Also contained in the invention are methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted proteins AAB25763-B25812. The proteins include signal pept
Included in the invention are a host cell containing one of the cDN
sequences, and a purified antibody capable of binding to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to sequences AAA87725-A87774 which encode human
                                                                                                                                                                           immunological
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Sequence 1701 BP; 499 A; 412 C; 372 G; 418 T; 0 other;

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Query Match

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Search completed: May 28, 2003, 00:05:43 Job time: 389.357 secs

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AF20811(	0.	AF20	F208110			1828 bp mRNA	linear PRI 17-JUL-	2-2000
DEFINITION	NO	Ношо		ens IL-17		nomolog precurs	(EVI27) mRNA	1
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SOURCE		Ното	sapi	ens.				
ORGANIS	Σ	Homo Euka Mamma	Homo sapiens Eukaryota, M Mammalia: Eu	o sapiens aryota, Metazoa, C malia, Rutheria: P	) a ;	hordata; Craniata; Ve rimates: Catarrhini:	Vertebrata; Euteleostomi : Hominidae: Homo.	mi;
REFERENCE		, Н	(bases	1 to 18	(58)			:
AUTHO		Tian, I	Shanor	Sawyer, ü	۳. د	Largaespada, D.A., J	enkins, N.A., Copeland, N	1, N.G.
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TRANAL Concodes a novel membrane protein with homology to the ILLY EVESTOR TO THE TRANAL CONCOGENIES IN (17), 2036-2103 (2000)  TRANAL CONCOGENIES IT (1828)  THE STATE A SUMMINICATION OF A KARRESS FOR MAGGING SCIENCES, 4301 W.  TRANS. SIMPLE A (14.NAV.) 1999 Mysloms and Transplantation Research Center, University of A Kransss for Madical Sciences, 4301 W.  TRANS. SILLILLE MOORE AND A MYSTILLY USA.  CENTER, SILLILLE MOORE A MYSTILLY USA.  CHARGES AND A MYSTILLY A MYSTILLY USA.  CHARGES A MYSTILLY A MYSTILLY A MYSTILLY MYSTILLY AND A MYSTILLY A MY	Best Loca	Matches		Db 1	Oy 61	Db 61	Qy 121	Db 121	Qy . 181	Db 181	Qy 241	Db 241	Qy 301	Db 301	Qy 361	Db 361	Oy 421	Db 421	Qy 481 (	Db 481 (	Oy 541	Db 541	Qy 601 (	Db 601 (	Qy 661	Db 661	Oy 721	Db 721	Qy 781 (	Db 781 (	Qy 841	Db 841	Qy 901	Db 901	Qy 961	Db 961	,
	encodes a novel membrane protein with homology to the	19 (17), 2098-2109	202/3223 10815801	2 (bases 1 to 1828) Shaughnessy, J.D. Jr.	Direct Submission Submitted (24-MANI-1999) Manipular and Transplantation Document	Center, University of Arkansa Ero Medical Sciences, 4301 W. Markham Ct Title Dock ab 722121 150		l. /org	/db_xref="taxon:9606" /chromosome="3"	/map="3p21" . 1. 1828	cotropic viral integration site 27	myeloid leukemias" 61514	/gene="BVI27" /note="BVI27A"	/codon_start=1 /product="IL-17 receptor homolog precursor"	/protein_id="AAF86051.1" /db_xref="G1:9246433"	/trānslation="mSLVLISLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD LRDLRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRC	NYTEAFOTOTRESGGKWIFSYIGFPVELNIVYFIGAHNIPNANMNEDGFSMSVNFTSP GCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTIIG	FSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPFFPTCGSDCIRHKGTVVLCPQTGV PPPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLWWRHERIKKTSFSTTTLLPPIKV	UVY IVBELCEHHIICIFIELOPHEKKEUN LEKWOKKLIABNGFVOWLAIOKKAADKV UVILSNDVNSVCDGTCGKSEGGENSCOLFFINLFOULFCDLREQIHLHKVVVYFRE IDTKDDVNSI,SVCDRVHRWIDEREFERILHVKOVVSCREGGENGGCTGFT,			/gene="EVI27" /product="IL-17	/gene="EVI27"	/noce="purative; giycosylation e 312314	/gene="EVI27" /note="putative; glycosylation	//14/6 /gene="EVI27" /note="murtative. n].rocer:]ation	480. 4 Parative, Gifcosylation 480. 481. (1997)	/yene="putative GSK3; phosphorylation sit /note="putative GSK3; phosphorylation sit so4 so6	/gene="EVI27" /note="mutative:	882995	<pre>/yene= byiz; /note="putative; transmembrane-region site 1299.1101</pre>	/gene="127" /note="nutative GSK3: phosphorylation site	16431644		site	a 438 c 397 g 445	

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
Tissue
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Homo sapiens, clone MGC:5245 IMAGE:2985728, mRNA, complete cds.
BC000980
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2042)
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Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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                    TTTCTCAGGTGTTTGAGCCACACACAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAG
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/protein_id="AAH00980.1"
/brotein_id="AAH00980.1"
/db xref="G1:12654319"
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LRDLAWEPVTTSVATGDYSILAWNVSWVLRABASIRLLikATKICYTGKSNFGSYSCYRC
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GCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVENNFTTFLGAHNIPNEDGPSMSVNFTSP
GCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVENNFTTFLGAHNIPNEDGPSMSVNFTSP
GCLDHIMKYKKCVKAGSLWDPNITACKKNEETVENNFTTFLGAHNIPUCPOTGV
PFPLDNNKSKPGGWLPLLLSLLVATWVLVAGIYLMRHRIKKTSFTTTLLPPIKV
LVVPBSEICFHHTICYFTFELQNHCRSEVILEKWQKKKIAEMSPVQWLATOKKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFRE
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         /organism="Homo sapiens"
/db xref=taxon:9606"
/clone="MGC:5245 IMAGE:2985728"
/tissue type="Cervix, carcinoma"
/clone lib="NIH MGC_12"
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NYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSP
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PFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMMRHERIKKTSFSTTTLLPPIKV
LVVYPSEICPHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKV
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1 (bases 1 to 1816)
Shi, Y., Ullrich, S.J., Zhang, J., Connolly, K., Grzegorzewski, K.J., Shi, Y., Ullrich, S.J., Wathen, K., Hodge, V., Fisher, C.L., Olsen, H., Ruben, S.M., Knyazev, I., Cho, Y.H., Kao, V., Wilkinson, K.A., Carrell, J.A. and Ebner, R.

A novel cytokine receptor-ligand pair Identification, molecular Jehrarcterization, and in vivo immunomodulatory activity
J. Biol. Chem. 275 (25), 19167-19176 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-DEC-1999) Molecular Biology, Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850, USA Location/Qualifiers
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                                                                                                   GCTGCTCCTTGTAGCCCCCCATGAGAAGGCAAGAGACCTTAAAGGCTTCCTATCCCACCA
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                      TTCTCCATGTCAAGCAGCAGCAGGAGGAAAAAAAAACATCACAAAGCCTGCCACGATGGCT
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Homo sapiens IL-17B receptor (IL17BR) mRNA, complete cds.
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/gene="IL17BR"
/note="similar to IL-17 receptor"
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db_xref="GI:8705222"
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/ LTAINS 1 at 10TH - MOSTALLESTABLICRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
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IDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"

397 c 377 g 382 t
Zhang, W. and Cao, X.
Direct Submission
Submitted (29-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R. China
Location/Qualifiers
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                                                                                                                                                                                                          product="putative cytokine receptor CRL4 precusor"
/protein id="AAK37428.1"
/db_xref="GI:13649477"
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Pred. No. 0;
0; Mismatches
                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens putative cytokine receptor CRL4 precusor mRNA,
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Homo sapiens
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SOURCE ORGANISM

KEYWORDS VERSION

REFERENCE

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AQAICLERLDRYCLGLQWTFSYIGFPVELNTYFIGANTPRANMEDGFSRAVRFTSP
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FSQVFEPHQKKQTRASVVIPVTGDSEGATVQLIFYFPTCGSDCIRHKGTVVLCPQTGV
PPPLDNNKSKPGGALPLLLSLLNATWVLVAGIYLDWRHERIKKTSFSTTTLLPPIKV
LVVYPSEICPHTICYFTFLQNNFCRSEVILEKWQKKKIAEMGFVQNLATQKKAADKV
VFLLSNDVNSVCDGTTGGKSGSPRSRNSQDLFPLFNLFCSDLASQIHLHKYVVVYFRE
IDTKDDYNALSVCPKYHLMKDATAPCAELLHVKQQVSAGKRSQACHDGCCSL"
                                       Craniata; Vertebrata; Euteleostomi;
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                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 2015)
Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and Nguyen, H.Q.
Il-17 receptor like molecules and uses thereof
Patent: Wo 0168705-A 4 20-SEP-2001;
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/ translation="WSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLOHDLIPGD
| translation="WSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLOHDLIPGD
| LRDLRVEPVTTSVATGDYSILAMVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRL
| LRDLRVCDLNLLGSSDRSAASRAAGTAGVGHQTWLIFVYFVEGGFTVLLVLNSS
| GCAD41MAXCDLNLLGSSDRAASRAGTAGVGHQTWLIFVYFVEGGFTVLLVLNSS
| AQA1CLPRLPKVJGLQWTFSYIGFPVELNTTYFYFTTPPLGMRYMALLIGGFSOVPETSP
| GCLD41MAYKXGTAASAVPTTPATGASTATTPLGMSTNAALIGGSTOVPTSP
| GCLD41MAYKXGTAASAVPTPTGAGGATVQLTPYFPTTTPLGMSTNAALIGGSTUV
| FSPLDNNKSKPGGWLPLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKV
| LVVYPSEICFHTTCYFTEFLQNHCRSEVILEKWQKKKIABWGPVQWLATOKKAADKV
| VFLLSNDNNSVGCTGGKSEGSPESNSQDLFPLAFNLFCSDLRSQIHLHKYVVVFRE
| IDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Il-17 molecules and uses thereof
Patent: WO 0208285-A 19 31-JAN-2002;
Amgen, Inc. (US)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1701)
dumas milne Edwards, J.B., Bougueleret, L. and Jobert, S.
Complementary dna's encoding proteins with signal peptides
Patent: WO 0100806-A 56 04-JAN-2001;
GENSET (FR)
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ACAAATACGTGGTGGTCTACTTTAGAGAGTTGATACAAAAGACGATTACAATGCTCTCA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3	3	86868686868686
CDS 2451402  // note="unnamed protein product"   // codon_start="   // codon_start="   // codon_start="   // protein_id="CAC25011.1"   // bx ref="G112406762"   // translation="MWTESYIGEVELNITYPFIGAHKIPNANMNEDGPSMSVNFTSPG CLDHIMKYKKKCKAGSEDNDNITACKKUBETVENTFTPLGNRYMALIQHSTIGF SOVFEPHOKKQTRASVVIPVTGDSEGATVQLTPFPTCGSDCIRHKGTVVLCPQTGVP FPLDNNKSKGRGMUPLLLISLILAWWAVLANFFTPREIKTFSTFTTPLGPSTTTLL VYPSELCFHHTTCYFPELCAMVAVLANFANTALVANFTREIK TANSSTGTTLLESLILAHTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHHTTCYFPELCHTCMONTALSVCPKXHIMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"   // polya signal 1669. 1674   // polya signal 1669. 1674   // DOLYA site 499 a 412 c 372 g 418 t  ORIGIN	Query Match         83.6%; Score 1527.8; DB 6; Length 1701;           Best Local Similarity         92.3%; Pred. No. 0;           Matches 1673; Conservative         0; Mismatches         12; Indels 128; Gaps         1;           Qy         1 CGGCGATGTCGTCGTGTGATAAGCTGGCGGTGTGCAGGAGCGCGTAACCCGAG         60         0	0y   301 GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACCAGAC

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FPLDNNKSKPGGWLPLLLSLLVATWVLVAGIYLAWRHERIKKTSFSTTTLLPPIKVL
VYPSEICFHTTICYFTFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQVKKAADKVU
FLLSNDVNSVCHGTGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVYFREI
DYKDDYNALSVCPRYTMKNDAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and Nguyen,H.Q.
Il-17 receptor like molecules and uses thereof Patent: WO 0168705-A 6 20-SEP-2001;
Amgen Inc. (US)
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/organism="Homo sapiens"
/organism="taxon:9606"
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/note="unnamed protein product"
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ATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATG
                                                                                           TTTCTCAGGTGTTTTGAGCCACACAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAG
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Oy 1561	61 ATTACAGGGAAAAAACGTGTGATGCTGAAGCTTACTATGCAGCCTACAAACAGCCTT 1620	qq	362 GG
Db 1477		λ	421 ATA
Qy 1621	21 AGTAATTAAAACATTTTATACCAATAAAATTTTCAAATATTACTAACTAATGTAGCATTA 1680	qa	422 ATP
Db 1537		δ	481 CAC
Qy 1681	31 ACTAACGATIGGAAACTACATITACAACTICAAAGCIGTITIATACATAGAAAICAATIA 1740	qq	482 CAC
Db 1597		δλ	541 TGT
Oy 1741	11 CAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCAATAAAGCATCTTC 1794	qa	542 TGT
Db 1657		ò	601 CA
		qa	602 CA
AX09242		δ	661 TTT
DEFINITION	AAU92426 1515 DP DNA 11Near PAT 23-MAK-2001 ION Sequence 157 from Patent WO0116318.	qa	662 TT
VERSION		ď	721 TG
SOURCE		qa	722 TGP
Organ		ò	781 GCG
REFERENCE	Mammaila; butheria; Filmares; cacarrilli; nomilizace; nomo.	qa	782 GCG
AUTHO		δδ	841 CTC
TITLE	wood,w.i. Secreted and transmembrane polypeptides and nucleic acids encoding	qu	842 CTC
JOURNAL	_	ò	901 TGC
FEATURES	Genentech, inc. (US) Location/Qualifiers	Ωp	902 TGC
õ	Source 1. 1215 /organism="Homo gapiens"	Qy	961 AGP
BASE COUNT	/ DX XIEI="CAXON:9606" JNT 404 a 384 c 363 g 364 t	qq	962 AGP
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· 참 옵	2 CGGCGATGTGGCTGCTGCTTAAGCCTGGCGCGCTGTGCAGGAGCGCCGTAACGAGGGGGGGG	qa	1082 GCP
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	AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG	Ωρ	1142 TGC
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97	181 CAGGGGCACTATTCAATTTTGATGAATGTTAAGCTGGGTACTCCGGGGCAGATGCCAGCATCC 240	ò t	1261
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	GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGCCAAAAGCAACTTCCAGTCCTACAGCT	. <b>q</b> а	
	GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT	ò	1381 CTC
2	301 GTGTCAGGTGCAATTACACACAGGCCTTCCAGACTCAGACCACTCTGGTGAAT 360 	qq	1382 CTC
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                                                    STGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 1515)

Chen, J., Filvaroff, E., Fong, S., Goddard, A., Godowski, P.J.,

Grimaldi, C.J., Gurney, A.L., Li, H., Hillan, K.J., Tumas, D., van
Lookeren, M., Vandlen, R.L., Watanabe, C.K., Williams, P.M., Wood, W.I.

and Yansura, D.G.

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                                                                              Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J. Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
                                                                                                                                                                                                                                                                            AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCCAGAGTGGATGCTACAACATG
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Bmail: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
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Full-length. CDNA libraries and normalization
Unpublished (2001)
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BM670929 UI-E-DW1-
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BI823321 603041231
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Minimum DB Maximum DB

Database

Result No.

Searched:

Sequence:

Run on:

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pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangeliferech.com URL: http://fulllength.invitrogen.com"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the
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/Anote="Organ: Fetal brain, Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies, addivision of Invitrogen 9800 Medical Center Drive Rockville fliang@lifetech.com URL:

Anaryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:

All 200 c 208 g 191 t 20 others
                                                                                                            AL535617 LTI FL013 FBrn1 Homo sapiens cDNA clone CSODF016YG03 5
prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .869
// Organism="Homo sapiens"
// Organism="taxon:9606"
/clone="CSODF016VG03"
// clone="LTI FL013 FBrn1"
// clone=lib="LTI FL013 FBrn1"
// ore varage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
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1 (bases 1 to 869)

1 (Aruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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2698 AATGTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATA
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                      AATGTAGCATTAACTAACGATTGGAAACCTCATTTCCAACCYCAAAGCTGTTTTATA
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Program for Rat Gene Discovery and Mapping
University of Iowa
University of Iowa
451 Bckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M. Researchers may obtain clones from Research
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye, Vector: pT7T3-Pac (Pharmacia) with a
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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/clone="UI-E-DW1-ahe-i-22-0-UI"
/clone_lib="UI-E-DW1"
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modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-E-DM1 is a normalized CDNA library containing the
following tissue(s): lens. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT713-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CGATTAGCGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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BM670929.1 GI:18980876
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Pred. No. 1.9e-106;
0; Mismatches 1; Indels 1;
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JOURNAL
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Ul="bM1-ahe-i-22-0-UI"
/clone="Ul="Ul-B-DM1"
/clone="Ul="Ul-B-DM1"
/clone="type="lens"
/dev stage="adult"
/lab_host="bH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT713-Pec (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
Ul-E-DM1 is a normalized cDNA library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with An oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT713-Pac
vector. The oligomoucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
761: 319 335 8250
Fax: 319 335 9565
Email: meoares@blue weeg uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics. (www.resgen.com).
Seg primer: M13 Forward
POLYA-Yes.
                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 657)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2190 AAGAAGGCAGCAGAAAAGTCGTCTTCCTTTTCCAATGACGTCAACAGTGTGTGCGAT 2249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2250 GGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTT 2309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           657 AAGAAGGCAGCAGACAAAAGTCGTCTTTCTTTTCCAATGACGTCAACAGTGTGTGCGGAT 598
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97044477
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TAG_TISSUE=human lens
TAG_SEQ=CGATTAGCGA"
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AUTHORS
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ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 641)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

IAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapba-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CDNA Library Arrayed by: Consortium/LLNL at:

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8419 row: a column: 04

High quality sequence stop: 639.
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab xref="taxon:9606"
/ Clone="InMAGE:3446667"
/ Coll line="MGC36"
/ Coll line="MGC36"
/ Inhoe="MGC36"
/ Note="Organ: cervix, Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life
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                                                                                GTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACC 2549
                                                                                                                                                                                                                                        2550 CATGAGAAGCAAGAGCCTTAAAGGCTTCCTATCCCACCAATTACAGGG-AAAAAACGTG 2608
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                                                                                                                                                                                                                                                                                CATGAGAAGCAAGAGACCTTAAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAAACGTG 238
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661 TTTCTCAGGTGTTTGAGCCACACAGAAGAACAACAAGGGGGGGCTTCAGTGGTGATTCCAG 720
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92.9%;
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Best Local Similarity 92.9
Matches 702; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 946)

S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1959)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The Technologies, Inc.

CDNA Library Arrayed by: The Technologies, Inc.

CDNA Library Arrayed by: The Technologies, Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
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                                                                                                                                   2244 TGCGATGGTACCTGTGGCAAGAGCGAGTCCCAGTGAGAACTCTCAAGACCTCTTC
                                                                                                                                                        CCCCTTGCCTTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATAC
                                                                                                                                                                                                                        121 CCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATAC
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                                                                                                                                                                                                                                                                      GTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGC
                                                                                                                                                                                                                                                                                                   181 GIGGIGGICTACTITAGAGAGATIGATACAAAAGACGATIACAGIGCICTCAGIGICIGC
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   641;
 Length
                                 Indels
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 DB 10;
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                                    4;
 Score 621.6; DB 10
Pred. No. 2.2e-103;
0; Mismatches 4;
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 21.8%;
99.2%;
Query Match 21.8
Best Local Similarity 99.2
Matches 635; Conservative
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BI823321
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/note=Torgan: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Site 1: NotI; Site 2: ECGRV (destroyed); RNA
source anonymous pool of emale brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECGRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NHH MGC Library."
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Pred. No. 4.4e-103;
0; Mismatches 4; Indels 50;
Found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                              /organism="Homo sapiens"
db xref="taxon:9606"
/clone="IMAGE:5182255"
/clone_lib="WHH MGC_115"
/lab_host="DH10B"
                             http://image.llnl.gov
Plate: LLAM11454 row: m column:
High quality sequence stop: 795.
Location/Qualifiers
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Homo sapiens
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602497744F1 NIH MGC_75 Homo sapiens cDNA clone IMAGE:4611491 S',
BG433769
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                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCKN1358 row: g column: 12
Plate: LLCKN1358 row: g column: 12
Plate: LLCKN1358 row: g column: 12
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 630)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2274 AGTCCCAGTGAGAACTCTCCAAGACCTCTTCCCCCTTTGAACCTTTTCTGCAGTGAT 2333
612 TTTCTCAGGTGTTTGAGCCACACAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAG 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626 TCCTTCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGAGCGAGGGC 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.9%; Score 598.2; DB 12; Length Best Local Similarity 97.9%; Pred. No. 4e-99; Matches 606; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="IMAGE:4611491"
/clone lib="NIH MGC 75"
/lab_host="DH10B (TI phage-resistant)"
                                                               672 TGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGA 707
                                            721 TGACTGGGGATAGTGAAGGTGCTACGGTGCAGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 610.
Location/Qualifiers
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                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                       RESULT 7
BG433769/c
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KEYWORDS
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AMY/ULD1 680 bp mRNA linear EST 01-JUN-2000 EST382232 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 680)
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446 AAAGACGATTACAATGCTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGGATGCCACT 387
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                                                     GCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGGTGTCAGCAGGAAAAAGATCACAA
                                                                                                                                                      GCCTGCCACGATGGCTGCTGCTTGTAGCCCCACCCATGAGAAGCAAGAGCCTTAAAG
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'I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
Quackenbush, J.
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Contact: John Quackenbush

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208
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/clone lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptSKm"
i 162 c 134 g 174 t 1 c
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Pred. No. 9.9e-97;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Conservative 0
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Plate: 273
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p mRNA linear EST 18-JAN-2000
sapiens cDNA clone IMAGE:2772915 3',
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
143 c 141 g 130 t l others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 510)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                  Score 554.2; DB 10; Length 561;
Pred. No. 4.3e-91;
0; Mismatches 4; Indels 0;
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Best Local Similarity 99.3%;
Matches 556; Conservative 0
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 561)
National lucitutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Other ESTS: bb40e05.x1
Contact: Robert Strausberg, Ph.D.
Email: capaba: remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution: Seq primer: -40RP from Gibco
High quality Sequence stop: 441.
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                          GAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGC
                                                                                                                                                       TCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGGCACTCCCAGTGAGAACTCTC
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 9 AW675096 LOCUS

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ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

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                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail:nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llh.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:772915"
/clone=lib="MXI CGAP_Kidl!"
/lab_host="MXI CGAP_Kidl!"
/lab_host="D4106"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not !; Site_2: Bco RI;
Plasmid DNA from the normalized library NCI CGAP_Kid3 was
prepared, and so circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonelDs 1322376-1323911, 1456007-1456775, and
1500552-150285). Subtraction by Bento Soares and M.
Fatima Bonaldo.
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Pred. No. 1.1e-80;
0; Mismatches 5; Indels
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Best Local Similarity 99.0%;
Matches 500; Conservative
  Jnpublished
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BF110326 509 bp mRNA linear EST 20-OCT-2000
Tan5f01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566736 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infooinage-Illi.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 470.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
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98.0%; Pred. No. 6.1e-80;
tive 0; Mismatches 10;
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,X., Lui,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2011)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujinan Human Genome Center at Shanghai
201203, P. R. China
121 86-21-50801911(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 bp mRNA linear EST 16-JAN-2
AV685699 GKC Homo sapiens cDNA clone GKCAAF09 5', mRNA sequence.
AV685699
502 CAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGAT 443
                                                                         442 TGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGA
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                                                TGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCCAAGTACCACTTCATGAAGGA
                                                                                                                                                                                                                                             262 CTTAAAGGCTTCCTATCCCAATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGI-CSAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 bp mRNA linear EST 27-JUL-2000 hx93h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3195409 3', BE465508
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 502)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                     2745
                                                                                                                                                                                                                      TGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATG 2805
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                                                                                                                     2686 ATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACTCAAAGC
                                                                                                                                                                   149 ATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGC
                         ACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAA
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/clone="IMAGE:3195409"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10B"
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Unpublished (1997)
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Matches 484; Conserv
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source

FEATURES

BASE COUNT ORIGIN

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE

JOURNAL

RESULT 12 BE466508/c DEFINITION EST 16-JAN-2002

Μ.D.

Emmert-Buck,

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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@lange.llnl.gov seq primer: -40UP from Gibco High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                  Anotes Organ: colon, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Pasamid DNA from the normalized library NCI CGAP Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone1Ds 105746-106125, and 1144884-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.,
Ph.D.
                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Co16"
/tissue_type="colon_tumor, RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                               1. .484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3323709"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 484)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
'note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Pred. No. 5.1e-77;
0; Mismatches 12;
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Best Local Similarity 84.8%;
Matches 599; Conservative
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                                                                           Score 475.2; DB 12;
Pred. No. 1.1e-76;
0; Mismatches 3;
  148 t
120 g
                                                                           Query Match

Best Local Similarity 99.4%;
Matches 477; Conservative 0
95 c
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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 873 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stops: 475.
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/Liscue Lype="colon"
/Liscue Lype="colon"
/Liscue Lype="colon"
/Liscue Lype="nHI08"
/Liscue Lype="color profiled polylinker; Site 1: Not I; Site 2: Eco RI; Ist strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of
     EST 18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 418)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AA514396 488 bp mRNA. linear EST 18-AUG-
nf57c01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924000 3'
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clone_lib="NCI_CGAP_Co3"
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GTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGA
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; Sequence 3, Application US/09778971
; Fatent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR PILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
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US-10-174-582-399

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US-10-176-783-399

US-10-176-982-399

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100.0%; Pred. No. 0;
ive 0; Mismatches
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; OTHER INFORMATĪON: cDNA of human Evi27
US-09-778-971-2
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  TYPE: DNA
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99, 241 90, 301 90, 301 90, 301 90, 301 90, 301 90, 481 90, 481 90, 481 90, 901 90, 901 901 901 901 901 901 901 901
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TACCCTT	CTGGCTG	TACGTGGT          TACGTGGT	ACAAAGTT             ACAAAGTT	GACTTTAC          GACTTTAC	GGTAGGGG          GGTAGGGG	TTGCTGTG         TTGCTGTG	TTTTCCTA          TTTTCCTA	AACAGGCG           AACAGGCG	CCTCCTGC          CCTCCTGC	GGAGGCACG           GGAGGCACG	GGTTCTTG          GGTTCTTG	ATTTCTTC	agcagaga          agcagaga	CTTCCTTC          CTTCCTTC	CAGTCCCA          CAGTCCCA	TCTAAGAA          TCTAAGAA	aaaagacg          aaaagacg	CACTGCTTTCT
	CTAAAGCA          CTAAAGCA	rerrrere         rerrrere	raacgtgt         raacgtgt	CTGGTTTTC             CTGGTTTTC	ACACTAGA(          ACACTAGA(	GTGAGATT         GTGAGATT	ACTCCATA          ACTCCATA	GCCCACA 	CTGCCTCT          CTGCCTCT	CTAATGTG          CTAATGTG	CCCATTAA(          CCCATTAA(	TTCACTGAA           TTCACTGAA	AAAGAAATI           \AAAGAAAATI	CAAAGTCGT(	accaacco          accaacco	CTGCAGTGAT 	TTGATAC         TTGATAC	atgccac
	SCATGTO	agaggaaa         agaggaaa	TATGTTAGT)            TATGTTAGT	TCGGGTCA         TCGGGTCA	SCATGACAA            SCATGACAA	AGAGTCTTG	CTCAGCTGA          CTCAGCTGA	GTTGTGCTCT             GTTGTGCTCT	gaggerreg          gaggerreg	SATCTAT	TACTGCCC         TACTGCCC	TTTGTTAC	GGCAGAAA          GGCAGAAA	CAGCAGAC         CAGCAGAC	GÍGGCAAGA          GTGGCAAGA		TTAGAGAGA           TTAGAGAGA	CATGAAGGATGC
	CAGGGACTTC	CTTTTTGE,             CTTTTTTGE	CGAACTGG          CGAACTGG	TGTGGGTCT          TGTGGGTCT	GAAAATGTGCATG             GAAAATGTGCATG	GAAGTA        GAAGTA	TGTTTTTC           TGTTTTTC	aggaacag          aggaacag	CAAGCCGG          CAAGCCGG	GGTGGCAGGG           GGTGGCAGG	CACCACAC!	TCACACAA         TCACACAA	TGAAAAGTC          TGAAAAGTC	AAGAAGG         AAGAAGG	GGTACCT         GGTACCT	GCCTTTAA(	GGTCTACT	TACCACT
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CACCAGAG	TAGACTTC         TAGACTTC	GGATCACTV          GGATCACTV	AGCCCTTTTAC                 AGCCCTTTTAC	CCGGGAGT	AGATGTGTGAC             AGATGTGTGAC	GGAA GGAA	ACTTTCT             ACTTTCT	CTGCATC         CTGCATC	GATAA        GATAA	seccaca        seccaca	AGACTTCCT'           AGACTTCCT'	CTGAAATAT            CTGAAATAT	gaagtgagg          gaagtgagg	Greectre           Greectre	CAACAGTG            CAACAGTG	AGACCTCT         AGACCTCT	GCACAAAT.	CAGTGTCT
	GGAGAACCA'           GGAGAACCA'	GCCAAGA         GCCAAGA	ATGACCT          ATGACCT	GTTCAGACC           GTTCAGACC	STTACA        STTACA	GCCAGAAAGAAC                 GCCAGAAAGAAC	ATGGTGTGA          ATGGTGTGA	rggcagcga          rggcagcga	CTTTCCCTCT             CTTTCCCTCT	rcrecresre          rcrecresr	GATCAAGA/          GATCAAGA/	TTACCCATC	CCATTGCAC            CCATTGCAC	ccagraca          ccagraca	CAATGACGT           CAATGACGT	GAACTCTCAA(           GAACTCTCAA	GATTCATCT	.aatgctci 
AGTG	7076   1077	AGGAA(       AGGAA(	AAGAT	TAGG      TAGG	GGCTTT(        GGCTTT(	CGAA(	ATGCA'       ATGCA'	CTTGTGGC          CTTGTGGC	TCCC:	TGTCT   TGTCT	AAAGO	TGGT   TGGT	AAAAC  - - -   - - -	TGGGT       TGGGT	7777C 	GTGAC       GTGAC	GCCAC 	ATTAC
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Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
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US-09-778-971-1
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Sequence 8062, Application US/09764891
Fublication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOG
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION NUMBER: US/09/764,891
FILE REPERIOR OF SEQ 1D NOS: 10231
NUMBER OF SEQ 1D NOS: 10231
SOFTWARR: PatentIn Ver. 2.0
SEQ 1D NO 8062
LENGTH: 32177
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41.3%; Score 1178.8; DB 9
Best Local Similarity 98.0%; Pred. No. 8.4e-305;
Matches 1203; Conservative 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; ORGANISM: Homo sapiens
US-09-764-891-8062
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AATGGCTGCTGACCTTCCAAAGCACTTTTTTATTTTCATTTTCTGTCACACACTCAGGG
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                  Query Match 37.7%; Score 1078; DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e-278; Matches 1078; Conservative 0; Mismatches 0;
         CURRENT APPLICATION NUMBER: US/09/778,971
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/180,374
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1827
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                  ; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of human Evi27
US-09-778-971-1
FILE REFERENCE: D6138
                                                                                                                      FEATURE:
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APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS FILE REFERENCE: DXO1170K
CURRENT PPLICATION NUMBER: US/09/863,818A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
PRIOR APPLICATION NUMBER: US 60/206,862
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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1530 CAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCT 1589
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                                                   GAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAA
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99.8%; Pred. No. 6.9e-269;
tive 0; Mismatches 2; Indels 0;
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US-09-863-818A-1
Sequence 1, Application US/09863818A
Publication No. US20030092881A1
GENERAL INFORMATION:
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Matches 1043; Conservative
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NAME/KEY: CDS

LOCATION: (4)..(1509)

OTHER INFORMATION:

NAME/KEY: mat_peptide

LOCATION: (46)..()

OTHER INFORMATION:

US-09-863-818A-1
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Gaps

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1779 CAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTT 1838
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                                                                                                                                                                                     3; Indels
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                                                                                                                                                     Query Match
Best Local Similarity 99.7
Matches 1042; Conservative
SEQ ID NO 17
LENGTH: 1841
TYPE: DNA
ORGANISM: Homo sapiens
                                                                               ) NAME/KEY: CDS
; LOCATION: (50)..(1555)
US-09-886-404-17
                                                                   FEATURE
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               CAGAAAAAAAAAAAAAAAGAGATGGGTCCAGTGGCTTGCCACTCAAAAGAAGGCA
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Patent No. US20020037524A1

GENERAL INFORMATION:
APPLICANT: Medlock, Eugene
APPLICANT: Yeh, Richard
APPLICANT: Silbiger, Scott M.
APPLICANT: Elliot, Garg S.
APPLICANT: Biloiger, Scott M.
APPLICANT: Biloiger, Scott M.
APPLICANT: Nguyen, Hung O.
APPLICANT: Nguyen, Hung O.
FILE REFERENCE: 01017/37128B
CURRENT APPLICATION NUMBER: US/09/886,404
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/810,384
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22
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US-09-886-404-17
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APPLICANT:
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                     1694 TITICAAATATTGCTAACTAATGTAGCATTAACTAAGGATTGGAAACTACATTTACAACT
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 TTTTCAAATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACT
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GENERAL INFORMATION:

APPLICANT: Wel, Richard

APPLICANT: Silbiger, Scott M.

APPLICANT: Silbiger, Scott M.

APPLICANT: Bliot, Gary S.

APPLICANT: Ding, Shugian

TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof

FILE REFERENCE: 01017/37128B

CURRENT APPLICATION NUMBER: US/09/886,404

FILE REPERENCE: 01017/37128B

CURRENT FILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-02-16

PRIOR PELICATION NUMBER: 60/266,159

PRIOR PELICATION NUMBER: 60/213,125

PRIOR PELICATION NUMBER: 60/213,125

PRIOR PELICATION NUMBER: 60/213,125

PRIOR PELICATION NUMBER: 60/213,125

SOFTWARE: PALCATION NUMBER: 60/213,125

SOFTWARE: PALCATION NUMBER: 2001-06-22

SOFTWARE: PALCATION NUMBER: 2001-06-22
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                                                                                                                                             GATAATGCAACAATAAAGCATCTTC 2823
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Patent No. US20020037524A1
GENERAL INFORMATION:
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Best Local Similarity 99.7
Matches 1042; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (50)..(1729)
US-09-886-404-19
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US-09-886-404-19
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ANT: Yansura, Daniel
OF INVENTION: 1L-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
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Patent No. US20020177188A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Hanzhong
Hillan, Kenneth J.
Hymowitz, Sarah G.
Tumas Daniel
Starovasnik, Melissa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VanLookeren, Menno
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Williams, P.Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
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Goddard, Audrey
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TITLE OF I
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CURRENT APPLICATION NUMBER: 195/99/97, 503
CURRENT PAPLICATION NUMBER: 105 605 674, 503
CURRENT PAPLICATION NUMBER: 105 60753, 646
PRIOR PALLICA DATE: 2001-06-05
PRIOR PALLICA DATE: 2001-01-28
PRIOR PALLICA DATE: 2000-01-128
PRIOR PALLICA DATE: 2000-01-21
PRIOR PALLING DATE: 1999-10-21
PRIOR PALLING DATE: 1999-10-23
PRIOR PALLING DATE: 1999-10-23
PRIOR PALLING DATE: 1999-0-21
PRIOR PALLING DATE: 2000-0-22
PRIOR PALLICATION WUMBER: US 09/140, 48
PRIOR PALLING DATE: 2000-0-12-0
PRIOR PALLING
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                                                               Length 1515;
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                                                             DB 9;
                                                                              Pred. No. 3.3e-194;
0; Mismatches 1;
                                                               Score 763.4;
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; Sequence 11, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
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Grimaldi, J.Christopher
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Goddard, Audrey
                                                                                             Matches 764; Conservative
                                                                                                                             1779 CAGCTGACTCCATATTT
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APPLICANT: Filvaroff,
APPLICANT: Goddard, Au
APPLICANT: Goddard, Au
APPLICANT: Godowski, P
APPLICANT: Grimaldi, J
TYPE: DNA
ORGANISM: Homo Sapien
US-09-874-503-11
                                                             Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: PCI/USOU/04341
PRIOR APPLICATION NUMBER: PCI/USOU/04341
PRIOR APPLICATION NUMBER: PCI/USOU/05601
PRIOR PELING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/USOU/0552
PRIOR PELING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/USOU/15264
PRIOR FILING DATE: 2000-08-24
PRIOR PELING DATE: 2000-08-24
PRIOR PELING DATE: 2000-01-10
PRIOR PELING DATE: 2000-11-10
PRIOR PELING DATE: 2000-11-00
PRIOR PELING DATE: 2000-11-00
PRIOR PELING DATE: 2000-12-01
PRIOR PELING DATE: 2000-12-01
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PRIOR PELING DATE: 2001-10-00
PRIOR PELING DATE: 2001-10-20
PRIOR PELING DATE: 2001-06-20
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SEQ ID NO 11
LENGTH: 1515
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Matches 764;
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; ORGANISM: HO
US-10-000-157-11
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                                                                                                                                                                                                                                                    APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
IITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381RIC1P4 (US)
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/000,157
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/085579
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FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/31274
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PRIOR PLING DATE: 1998-07-0337)
PRIOR PLING DATE: 1998-10-23
PRIOR PLING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 2000-01-11
PRIOR PLING DATE: 2000-01-11
PRIOR PLING DATE: 2000-01-11
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-11-28
PRIOR PLING DATE: 2000-11-28
PRIOR PLING DATE: 2000-10-26
PRIOR PR
                                                                                                      Starovasnik, Melissa
VanLookeren, Menno
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Williams, P.Mickey
Wood, William
            illan, Kenneth J.
                                                                                                                                                                   Vandlen, Richard
                                                                          Vumas, Daniel
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Gaps

0;

Length 1515; Indels

Score 763.4; DB 9; Pred. No. 3.3e-194; 0; Mismatches

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APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff,Ellen
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Hillan, Kenneth
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 157
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Pred. No. 3.3e-194;
0; Mismatches 1;
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Grimaldi, Christopher J.
Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.9%;
Matches 764; Conservative
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; ORGANISM: Homo Sapien
US-10-063-547-157
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APPLICANT: WAGGG, MILLIAM,

APPLICANT: WAGGG, MILLIAM,

TITLE OF INVENTION: IL-17 HOWOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REPRENCE: PISSIRICILIU (US)

CURRENT APPLICATION NUMBER: US 09/311,832

PRIOR PLING DATE: 1999-12-23

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 2000-01-11

PRIOR PLING DATE: 2000-01-11

PRIOR PLING DATE: 2000-02-18

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-03

PRIOR PLING DATE: 2000-03-03

PRIOR PLING DATE: 2000-03-03

PRIOR PLING DATE: 2000-03-03

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

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Publication No. US20030008815A1
GENERAL INFORMATION:
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Williams, P.Mickey
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Similarity
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Pred. No. 3.3e-194;
0; Mismatches 1; Indels 0;
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      PRIOR FILING DATE: 2000-06-02
PRIOR PLING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR PILING DATE: 2000-08-22
PRIOR PELING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-10-34
PRIOR PILING DATE: 2000-10-34
PRIOR FILING DATE: 2000-11-10
PRIOR PILING DATE: 2000-11-10
 APPLICATION NUMBER: PCT/US00/15264
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Best Local Similarity 99.9%;
Matches 764; Conservative
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CORGANISM: Homo Sapien
US-09-747-259-11
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TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 202-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 399
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Pred. No: 3.3e-194;
0; Mismatches 1;
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Wood, William I.
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Smith, Victoria
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ORGANISM: Homo Sapien
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26.7%; Score 763.4; DB 9; 99.9%; Pred. No. 3.3e-194; rative 0; Mismatches 1;
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GORGANISM: Homo Sapien
US-10-063-616-157
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Swith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Applicant: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/176,758
CURRENT APPLICATION NUMBER: US/10/176,758
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1231 GGCAAGAGGGAGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAAC 1290
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Publication No. US20030008353A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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; ORGANISM: Homo Sapien
US-10-176-758-399
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US-10-176-758-399
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APPLICANT: Eaton, Dan L.
APPLICANT: Elvaroff, Ellen
APPLICANT: Elvaroff, Ellen
APPLICANT: Gerrieten, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimald, Christopher J.
APPLICANT: Grimald, Christopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wa 2198 1170 2258 1290 2498 1350 2438 1411 ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGGGGGTGTCAGCA 1470 1779 CAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTT 1838 1899 GGCTGGCTGCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGG 1958 Gaps 1231 GGCAAGAGGGGGGGGGGCCCCAGTGAGAACTCTCCAAGACCTCTCCCCCTTGCCTTTAAC 751 CAGCTGACTCCATATTTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTT CTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTTTT AGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACTTC 1351 AGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTC ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCA 1051 TGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGG GGCAAGAGCGAGGCCAGTCCCAGTGAAACTCTCAAGACCTCTTCCCCCTTGCCTTTAAC CTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTT ô Length 1515; Indels 1471 GGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAG 1515 2499 GGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAG 2543 8

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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood William I.
APPLICANT: Wood William I.
APPLICANT: APPLICANT: ANOTON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND CURRENT APPLICATION NUMBER: US/10/175, 737
CURRENT PILLIA DATE: 2002-06-19
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 399
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APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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; ORGANISM: Homo
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PUDIcation No. US20030023042A1
GENERAL INFORMATION:
APPLICANT: Filvaroff,Ellen
APPLICANT: Goddard,Audrev
APPLICANT: Godowski,Paul J.
APPLICANT: Godowski,Mustin L.
APPLICANT: Watanabe,Colin K.
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      DB 9;
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CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 157
LENGTH: 1515
TYPE: DNA
TYPE: DNA
CRGANISM: Homo Sapien
US-10-063-502-157
                                                                                                                                                                DB 9;
                                                                                                                                                             Score 763.4; DB 9;
Pred. No. 3.3e-194;
0; Mismatches 1;
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Job time : 422.392 secs
                                                                                                                                                               26.78;
                                                                                                                                                            Query Match
Best Local Similarity 99.9°
Matches 764; Conservative
FILE REFERENCE: P3230R1C1
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Score 53; DB 2; ]
Pred. No. 0.00027;
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 6243 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 3770..4013
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Best Local Similarity
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Compugen Ltd.
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US-09-005-051-26
US-08-242-677-1
US-09-014-969-14
US-09-247-373B-25
US-09-296-715-25
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US-08-655-352-10
US-09-258-016-10
US-09-257-825B-10
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-861-458C-4
US-08-747-221B-24
US-08-747-221B-26
US-09-005-051-24
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US-08-998-416-595
US-08-545-196B-10
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US-09-227-357-139
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US-09-665-309-1
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GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
                                                            Sequence 13,
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      Sequence Sequence S
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APPLICANT: Johnson, Eric A.
APPLICANT: Bradshaw, Marite
APPLICANT: Rood, Julian
TITLE OF INVENTION: Expression System for Clostridium; TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady; STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
US-09-227-357-31

US-09-465-558-59

US-08-764-100-13

US-08-764-100-13

US-08-764-100-2

US-08-764-100-2

US-08-764-100-10

US-08-769-15

US-08-909-965C-8

US-08-909-965C-8

US-08-909-965C-8

US-08-909-965C-8

US-08-909-965C-8

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US-08-909-965C-8
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CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET WUMBER: 960296.95238
TELECOMMUNICATION INFORMATION:
TRIEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Length 6243;

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Matches 113; Conservative
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APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
CORRESPONDENCES: 45
CORRESPONDENCE ADDRESS:
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                                         2580 TATCCCACCATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTAC 2639
                                                                                                                          2640 AAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATATTTACTAACTAA 2699
                                                                                                                                                      2700 TGTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAG 2759
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  0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
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COUNTRY: US
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
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NAME: Israelsen, Ned
REGISTRATION UNDRERS: 29,655
REFERENCE/DOCKET UNDRERS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%;
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Chitnis, Chetan
Miller, Louis H.
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TYPE: nucleic acid
STRANDEDNESS: single
  Matches 137; Conservative
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Best Local Similarity
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US-08-487-826B-13
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Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-coding sequence (not including
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ADDRESSEE: Whinston, LLP
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REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECHONE: (503) 226-7391
FELEPHONE: (503) 226-7391
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MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM FC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WOrdPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 80
CLASSIFICATION OF
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-655-352-10
; Sequence 10, Application US/08655352
; Sequent No. 6077991
; GENERAL INFORMATION:
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STRANDEDNESS: double stranded
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nucleotides 20-1570
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US-08-655-352-10
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MARYLAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                            2748 TTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCA 2807
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Query Match
1.7%; Score 49.8; DB 3; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.001;
Matches 72; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%; Score 49.8; DB 4; Length 1776; 66.1%; Pred. No. 0.001; cive 0; Mismatches 37; Indels 0
                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
DESCRIPTION: sequence
                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09258016
Sequence 10, Application US/09258016
Patent No. 6362395
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: protein-coding sequence (not including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston, LLP STREET: One World Trade Center STREET: 121 S.W. Salmon Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTONBY AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
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: United States of America
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STRANDEDNESS: double stranded
TOPOLOGY: linear
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nucleotides 20-1570
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Best Local Similarity 66.1
Matches 72; Conservative
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STATE: Oregon
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CLASSIFICATION:
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US-09-258-016-10
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APPLICANT: Patil, Shameekumar APPLICANT: Patil, Shameekumar APPLICANT: Takezawa, Daisuke TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants TILE OF INVENTION COMPOSITIONS OF STATEMENT APPLICATION NUMBER: US/09/257,825B CURRENT APPLICATION NUMBER: US 08/655,352 PRIOR PILING DATE: 1996-05-23 PRIOR PILING DATE: 1996-05-23 PRIOR PILING DATE: 1996-03-28 PRIOR PILING DATE: 1996-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2748 TITTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCA 2807
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
STREESSEE: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.7%; Score 49.8; Di
Best Local Similarity 66.1%; Pred. No. 0.00;
Matches 72; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
                                                                           RESULT 5
US-09-257-825B-10
Sequence 10, Application US/09257825B
; Patent No. 6403352
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Poovaiah, Bachettira W.
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SOFTWARE: Patentin version 3.1
SEQ ID NO 10
EBNGTH: 1776
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NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Nicotiana tabacum
US-09-257-825B-10
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single
                       ; TOPOLOGY: linear
US-07-861-458C-4
      STRANDEDNESS:
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US-08-747-221B-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Pred. No. 0.00046;
0; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/861,458C
FILING DATE: 04/01/92
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATMOMBLY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATMOMBLY APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marchionni, Mark Andrew
APPLICANT: Marchionni, Mark Andrew
TTLE OF INVENTION: HOWOLGGY CLONING
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04585/014001
                                                                                                                                             MOLECULE TYPE: oligodeoxynucleotide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/07861458C
Patent No. 6232061
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REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.6%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617) 542-8906
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1100
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 02110-2804
                                                                                                                                                                   HYPOTHETICAL: NO ANTI-SENSE: YES
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                                                                LENGTH:
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                                                                                                        2771 AGCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAA 2830
                                                                                                                                                           2688 TATGGATTAATGTCAACATGTAAAATACAAATGCGGTTGTTAAAAATAATCTGTATTAAA 2747
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                     .;
0
     Length 1100;
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                                                     Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
Query Match 1.7%; Score 49.2; DB 4; 1
Best Local Similarity 73.3%; Pred. No. 0.0012;
Matches 63; Conservative 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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; Patent No. 6063610
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CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION VINDRER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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Best Local Similarity 58.69
Matches 85, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99..1889
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TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES ADDRESS:
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CITY: Fort Collins
STATE: Colorado
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SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
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          Nancy
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99..1889
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-005-051-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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2772 GCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAA 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2712 TAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTATACATAGAAATCAATTACA 2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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15-26/C
15-26-747-221B-26/C
15-26-747-
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1.7%; Score 49; DB 3; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0022;
Matches 85; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
PPERFECTION NUMBER: 77,459
                                                                     2832 AAAAAAAAAAAAAAAAAAAAAAA 2856
                                                                                                                                      2808 AAAAAAAAAAAAAAAAAAAAA 2832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2832 AAAAAAAAAAAAAAAAAAAAAAAA 2856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
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Patent No. 6291222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 ААААААААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FC
FELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 2836 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2836 nucleoti
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-747-221B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-005-051-24
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2712 TAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACA 2771
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Sequence 26, Application US/09005051

Sequence 26, Application US/09005051

Patent No. 6291222

APPLICANT: Silver, Gary W.

APPLICANT: Wisnewski, Nancy

TITLE OF INVENTION: No. 62912222

TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heska Corporation

ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                         ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
TELEPROMENICATION INFORMATION:
TELEPROMENICATION INFORMATION:
TELEPROMENICATION INFORMATION:
TELEPROMENICATION 1900,493-7272
TELEPROMENICATION 1900,493-7272
ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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1825 Sharp Point Drive

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OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
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0.0031;
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Pred. No. 0.00
0; Mismatches
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APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Reche, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spanlding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEIT
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc
STREET: RECHEAT OF A CAMBRIGGEPARK Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
                                     CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: MAYfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMUNICATION INFORMATION:
TELEPHONE: 713-78-1400
TELEFAX: 713-78-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5173 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.7%;
Best Local Similarity 69.1%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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COUNTRY: U.:
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                               ;
LOCATION:
US-08-242-677-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2772 GCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAAA 2831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 TATGGATTAATGTCAACATGTAAAATACAAATGCGGTTGTTAAAAATAATCTGTATTAAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squence 1, Application US/08242677
; Sequence 1, Application US/08242677
; Patent No. 567743
; GENERAL INFORMATION:
    APPLICANT: Gaynor, Richard B
    APPLICANT: Gaynor, Richard B
    APPLICANT: Wo, FOON W.
    TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
    TITLE OF INVENTION: Treatment of AIDS
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TX
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%; Score 49; DB 4; Length 2836;
58.6%; Pred. No. 0.0022;
tive 0; Mismatches 60; Indels
                                                             ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                              PILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/747,221
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser/ Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEBRANE, 970/493-7272
TELEBRANE: 970/493-505
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
TEMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.69
Matches 85, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-09-005-051-26
                     Colorado
: USA
                                                          80525
                  STATE: COCONTRY:
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2760 AAATCAATTACAGCTTTAAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCAT 2819
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          APPLICATION NUMBER: US/08/242,677 FILING DATE:
CURRENT APPLICATION DATA:
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PROTEINS AND POLYNUCLEOTIDES
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Search completed: May 28, 2003, 10:21:46
Job time : 242.942 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2683 CAAATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2743 AGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.4; DB 2; Length 2447;
Pred. No. 0.003;
0; Mismatches 116; Indels 0
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APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF SEQUENCES: 32
CORRESPONDERSES:
ADDRESSEE: E.I. DU FONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,747
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STREET: 1007 MARKET STREET
CITY: ILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
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; Sequence 25, Application US/08924747
; Patent No. 6063570
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NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.4%;
Matches 118; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                               nucleic acid
EDNESS: double
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CLASSIFICATION: 435
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TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REPERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.2; DB 4; Length 991;
Pred. No. 0.0021;
0; Mismatches 28; Indels
                                                                                               Length 991;
                                                                                            Score 48.2; DB 3;
Pred. No. 0.0021;
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Best Local Similarity 69.9
Matches 65; Conservative
; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
US-08-924-747-25
                                                                                                        Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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; ORGANISM: SOYBEAN
US-09-247-373B-25
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-247-373B-25
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                                                                                               Query Match
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PRO5801 CDNA IL-17RH CDNA

DCRS6 revers interleukin-

cDNA encodin

Scoring table:

Searched:

Database

Sequence:

Title:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human interleukin-17 receptor related protein (Evi27) encoding cDNA #2.
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Human
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Human
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6..872
/*tag= a
/product= "Human Evi27 protein"
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AAS46124
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AAZ52036
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AAX12137
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ABL70352
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(UYAR-) UNIV ARKANSAS
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                                                                                                                                                                                      Description
            GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Listing first 45 summaries
                                                         nucleic search, using sw model
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Result Š.

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Shaughnessy JD;

The present sequence is a cDNA encoding human interleukin (IL)-17 receptor related protein (Evi27). Human Evi27 gene was mapped to chromosome 3p21. Evi27 is a common site of retroviral integration in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful as antisense molecules to inhibit Evi27 protein or for chromosomal mapping or mutational analysis of Evi27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic calls. Hence modulating the expression of Evi27 at the RNA or protein level is used in the treatment of diseases such as cancer acids encoding an interleukin (IL)-17 receptor related use as a marker for leukemia Claim 1a; Page 75-76; 87pp; English. or autoimmune diseases. WPI; 2001-496920/54 P-PSDB; AAE07161 New nucleic protein for 

Sequence 2856 BP; 793 A; 655 C; 682 G; 725 T; 1 other;

ö AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 600 600 9 9 9 Gaps CGGCGATGTCGCTCGTGCTGATAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAG CGGCGATGTCGCTCGTGCTGATAAGCCTGGCCGCGCTTGCAGGAGCGCCGTACCCCGAG AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCCAGAGTGGATGCTACAACATG ATCTAATCCCCGGAGAGTTGAGGGACCTCCCGAGTAGAACCTGTTACAACTAGTGTTGCAA TGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCA CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATGGGT **ATCTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAA** CAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC CAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT TGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTCA GCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCT GTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAAT GTGTGAGGTGCAATTACACAGAGGCCTTTCCAGACTCAGACCCACACTCTGGTGGTAAAT GGACATTITICCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCC GGACATTTTCCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCC ATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCT ; 22; Length 2856; Indels ; 0 DB ; Score 2855; I; Pred. No. 0; 0; Mismatches Query Match 100.0%; Best Local Similarity 100.0%; Matches 2856; Conservative 0; Н 61 -61 121 121 181 181 421 241 241 301 361 481 541 301 361 421 481 541 601 움 ઠે g ठ a δ g ò 셤 ò a ò 엄 ò g ò 셤 ò a 8 ઠે

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel human interleukin receptor-ligand (IL-17B and IL17BR) 32.56. The product of the invention can be used treat several diseases, such as rheumatoid arthritis, inflammation, immunological disease, various tumours and development disturbance. Sequence encodes the human interleukin receptor-ligand (IL-17B and IL17BR) 32.56 described in the method of the invention.
                                                                                                                                                                                                                                                                                                                         "interleukin receptor-ligand (IL-17B and IL17BR) 32.56"
                                                                                                                                                                                              Human; interleukin receptor-ligand (IL-17B and IL17BR) 32.56;
rheumatoid arthritis; inflammation; immunological disease; tumour;
development disturbance; gene; ss.
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Best Local Similarity 99.4%;
Matches 2672; Conservative
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antihalammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antitalhergic; antidiacheric; antiuloer; anticonvulsant; antimogal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
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2401 ATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACTTCATGAAGGATGCCACTGCTTTCT
                                                                            ACGATGGTTGCTGCTCCTTGTAGCCCCCCTTGAGAGAAGCAAGAGACCTTAAAAGGCTTCCT
                                                                                                   ATCCCACCAATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACA
                                                                                                              ATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACA
         ATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCT
                                 GTGCAGAACTTCTCCATGTCAAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCC
                                                  Grecagaactrorocargreaagcagcaggrercaggaagaaaaagarcacaagccrece
                                                                  ACGATGGCTGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCT
                                                                                                                                     AACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATAT 2689
                                                                                                                                               AACAGCCTTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATAT 2725
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            08-NOV-2000;
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -The invention relates to novel genes (ABA11004-ABA21534) and proteins Disclosure; SEQ ID NO 10824; 1701pp + Sequence Listing; English

The invention is takens to invert gauss (account).

(ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disbease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CC Printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

41.3%; Score 1178.8; DB 22; Length 32177; 98.0%; Pred. No. 4.7e-269; Sequence 32177 BP; 8826 A; 6801 C; 7130 G; 9420 T; 0 other; Query Match Best Local Similarity

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24433 24133 24073 24013 24552 TCTCTCTCTTTAAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTG 24493 23594 23834 1022 1082 1142 1262 23774 1502 1322 1442 842 TCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTG 24492 ACTGGGGATAGTGAAGGTGCTACGGTGCAGGTAAAGTTCAGTGAGCTGCTCTGGGGAGGG 24432 AAGGGACATAGAAGACTGTTCCATCATTCATTGCTTTTAAGGATGAGTTCTCTCTTGTCA 24012 CCTCTCAGTATGTCTCTTTCAACTCTAGTTTTTGAGGTGGGGACACAGGAGGTCCAGT-G GGACACAGCCACTCCCCAAAGAATAAGGAACTTCCATGCTTCATTCCCTGGCATAAAAG GGACACAGCCACTCCCCAAAGAGTAAGGAGCTTCCATGCTTCATTCCCTGGCATAAAAG TGGAGAACCATAGACTTCCCTTACTACAGGGACTTGCATGTCCTAAAAGCACTGGCTGAAG GAAGCCAAGAGGATCACTGCTGCTTTTTTTCTAGAGGAAATGTTTGTCTACGTGGTAA GATATGACCTAGCCCTTTAGGTAAGCGAACTGGTATGTTAGTAACGTGTACAAGTTTA 23533 AAGCCAGAAAGAAGGAAGTTTTGGCTGAAGTAGGAGTCTTGGTGAGATTTTGCTCTGAT AAGGGACATAGAAGACTGTTCCATTCATTGCTTTTAAGGATGAGTTCTCTTTTGTCA AATGCACTICTGCCAGCAGACACCCAGTIAAGTGGCGTTCATGGGGGTTCTTTCGCTGCAG CCTCCACCGTGCTGAGGTCAGGAGGCCGACGTGGCAGTTGTGGTCCCTTTTGCTTGTATT CCTCCACCGTGCTGAGGTCAGGAGGCCGACGTGGCAGTTGTGGTTCTTTTGCTTGTATT AATGGCTGCTGACCTTCCAAAGCACTTTTTATTTTCATTTTCTGTCACAGACACTCAGGG ATAGCAGTACCATTTTACTTCCGCAAGCCTTTAACTGCAAGATGAAGCTGCAAAAGGGTTT GAAATGGGAAGGTTTGAGTTCCAGGCAGCGTATGAACTCTGGAGAGGGGCTGCCAGTCCT CTCTGGGCCGCAGCGGACCCCAGCTGGAACACAGGAAGTTGGAGCAGTAGGTGCTCCTTCA crcregeccecaececaecregaacacacaecaecaerregaecregaecrecrecae CCTCTCAGTATGTCTCTTTCAACTCTAGTTTTTGAAGTGGGGACACAGGAAGTCCAGTGG TGNTCAAACACACCAGAGGGGGAGGCACCAGCCAGGGTATGATGATGGGTACTACCCCTTTTC TGGAGAACCATAGACTTCCCTTACTACAGGGACTTGCATGTCCTAAAGCACTGGCTGAAG GAAGCCAAGAGGATCACTGCTGCTCCTTTTTTGTAGAGGAAATGTTTGTGTACGTGGTAA GATATGACCTAGCCCTTTTAGGTAAGCGAACTGGTATGTTAGTAACGTGTACAAAGTTTA GGTTCAGACCCCGGGAGTCTTGGGCATGTGGGTCTCGGGTCACTGGTTTGACTTTAGGG GGTTCAGACCCCGGGAGTCTTGGGCCACGTGGTCTCGGGTCACTGGTTTTGACTTTAGGG **AAGCCAGAAAGAAGGGAAGTTTTGGCTGAAGTAGGAGTCTTGGTGAGATTTTTGCTGTGAT** 24132 GAAATGGGAAGGTTTGAGTTCCAGGCAGCGTATGAACTCTGGAGAGGGGCTGCCAGTCCT CTTTGTTACAGATGTGTGACCAAGGGGAAAATGTGCATGACAACACTAGAGGTAGGGGCG 663 723 963 843 903 24372 24252 1083 24072 1383 783 24312 1023 24192 1143 1263 23833 1443 1503 1563 1683 1203 23953 1323 23893 1623 23773 23713 23653 23593 임 Š ò 셤 ò g ò g à q ò a ò 셤 ò g ò 셤 ò 원 ò g ò В ò 셤 ò g ò 셤 à 셤 ò 셤 ò

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Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse; act; dog; chicken; sheep; immunosuppressive; antiarthrific; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; fungal infection; viral infection; ocular disorder; eaptrator; pastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
     Human cytoskeletal element-related polypeptide encoding genomic DNA #15.
                                                       23413 TGTGGCAGCGACTCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGGGTC 23354
                                          TGTGGCAGCGACTGCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTC
                                                                                        CCTTTCCCTCTGGATAACAGTAGTGC 23327
                                                                              CCTTTCCCTCTGGATAACAACAAAGC 1889
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AAS29828/c
ID AAS29828 standard; DNA; 32177
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2000US-0189874.
2000US-0190076.
2000US-0198123.
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17-MAR-2000;
18-APR-2000;
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Sequences AAS29814-AAS29838 represent genomic DNA molecules, which encode the cytoskeletal element-related polypeptides of the invention.

Cytoskeletal polypeptides and their associated polymucleotides are useful cin the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in a cytoskeletal polymucleotide. The treatable disorders include autoimmume diseases such as rheumatoid architeis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as carefac arriest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, coular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal cdisorders such as premature labour and infertility, gastrointestinal cdisorders such as gremature labour and infertility, gastrointestinal colonypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          el isolated human cytoskeletal element-related polypeptide useful diagnosis/treatment of neoplastic disorders, disorders associated n neural transmission, chromosomal abnormalities, autoimmune
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                                             2000US-0249208.
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Score 1178.8; DB 22; Length 32177; Pred. No. 4.7e-269; 41.3%; 98.0%; Best Local Similarity Query Match

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2000US-0231414.
2000US-0232080.
2000US-0232081.
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                                                                                                                                                             Human, reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
TGTGGCAGCGACTCCGACATAAAGGAACAGTTGTGCTCTGCCCCACAAACAGGCGTC
                                                                                                                                                Human reproductive system related antigen DNA SEQ ID NO:
                                                                CCTTTCCCTCTGGATAACAACAAAGC 1889
                                                                                        RESULT 5
AALO5374/c
ID AALO5374 standard; DNA; 32177 BP
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2000US-0189874.
2000US-0190076.
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Human, interleukin-17 receptor related protein, IL-17; chromosome 3p21;
Evi27; retroviral integration; chromosomal mapping; mutational analysis;
                                                                                                                                                                                                                                                                                       Human interleukin-17 receptor related protein (Evi27) encoding cDNA #1.
                                                                                                                                                                CTCTGGGCCGCAGCGGACCCAGCTGGAACTTGGAAGTTGGAGCAGTAGGTGCTCCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24552 TCTCTCTCTTTAAGCCACACACAGAAAAAAAAAAAAGCGAGCTTCAGTGGTGATTCCAGTG 24493
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98.0%; Pred. No. 4.7e-269;
ative 0; Mismatches 23; Indels 1 63
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200005-0249297.
200005-0249300.
200005-0250160.
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2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0251869.
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Best Local Similarity 98.0
Matches 1203; Conservative
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septic shock; impotence; ss.
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   cytokine; IL-8; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2018
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                                                                                                                                             /product= "Human mature Evi27 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 1078; DB 22;
100.0%; Pred. No. 1.3e-245;
ive 0; Mismatches 0;
             disease;
myeloid leukaemia; proinflammatory
tic cell; cancer; autoimmune disease
                                                                           /*tag= a
/product= "Human Evi27 protein"
                                                       iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Claim 1a; Page 74-75; 87pp; English
                                                                                                                                                                                                             02-FEB-2001; 2001WO-US03518
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             haematopoietic
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Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
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                                                                                                                                                                                                                                                                Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping procedures -
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Pred. No. 2.8e-239;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                        Claim 1; Page 221-223; 306pp; English.
                                                                                                                                                                                            Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.8%;
                                                                                              99WO-IB02058
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99US-0141032
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Matches 1056; Conservative
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P-PSDB; AAB25795.
                                       WO200037491-A2
                                                                                                                                                                 (GEST ) GENSET
              Homo sapiens
                                                                                            20-DEC-1999;
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25-JUN-1999;
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The invention relates to primate and rodent DNAX cytokine receptor subbunit (DCRS) polypeptides and the polymucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, eg., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rtokine receptor subunit 6; DCRS6; phosphate labelling; protein therapy; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
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               CAAGAGACCTTAAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATGCT
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                                              CAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAACGTGTGATGATCCT
                                                                                                                                                                                                                                                                                           Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA
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/product= "Human DCRS6"
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                                                                                                                    Secreted proteins and the nucleic acids encoding the therapy and for detecting similar sequences in
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ive 0; Mismatches 8;
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A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents CDNA encoding the human
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                                                                                                                       DB 24; Length 1796;
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                                                                                           Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;
                                                                                                                                      Pred. No. 4.9e-237;
0; Mismatches 2;
                                                                                                                       36.5%; Score 1041.8; 99.8%; Pred. No. 4.9e
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The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is sone such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obseity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), hone disease (e.g. obteoporosis), vascular system disorders (e.g. ischammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, IL-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
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"Human IL-17 receptor-like protein #3"
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                                    Score 1040.2; DB 24
Pred. No. 1.1e-236;
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Best Local Similarity 99.7%;
Matches 1042; Conservative
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Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; ecema; sepsis; psoriasis; wound healing; osteopoxosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
1626 TCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTT 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia, retinal neuropathy, infertility, miscarriage, inflammation, cancer, diabetes, ds.
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                                                                                               1686 GATAATGCAACAATAAAGCATCTTC 1710
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02-FEB-2001; 2001US-266159P.
16-MAR-2001; 2001US-0810384.
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            (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma leukaemia); reproductive (infertility, miscarriage, endometriosis), eye (blindness, retinal neuropathy) and treatment of diseases involving inflammation. The present sequence is human Interleukin-17 receptor B-2
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                                                                                                                                            Score 1040.2; DB 24
Pred. No. 1.2e-236;
0; Mismatches 3;
wound healing); kidney
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Best Local Similarity 99.7%;
Matches 1042; Conservative
                                                                                     (IL-17RB-2) DNA
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The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), sin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g.
                                                                                                                                                                                                                                                                                                                                             Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
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diagnosing, ameliorating or
(e.g. psoriatic arthritis) and
                    TTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACT
TTTTCAAATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACT
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                                                          TCAAAGCTGTTTTATACATAGAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTT
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                                                                                                                                                                                                                                                                                                                  Human IL-17 receptor like protein #1 coding sequence.
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50..1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three human nucleic acids encoding polypeptides, useful for treating, preventing immune system disorders infections (e.g. viral infections)
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eye disorders, reproductive disorders, tumours and
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Best Local Similarity 99.7%; Pred. No. 1.2e-236;
Matches 1042; Conservative 0; Mismatches 3;
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Human; interleukin-17 receptor B-3; IL-117RB-3; immune system dysfunction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukaemia; retinal neuropathy; infertility; miscarriage; inflammation; cancer; diabetes; ds.
                                                               1813
                                 1754 TCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTT
TCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTT
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02-FEB-2001; 2001US-266159P.
16-MAR-2001; 2001US-0810384.
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                 (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin pooriasis, eczema, wound healing); kidney (glomerulonephritis); bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma leukaemia); reproductive (infertility, miscarriage, endometriosis), eye (blindness, retinal neuropathy) and treatment of diseases involving inflammation. The present sequence is human Interleukin-17 receptor B-3 (IL-17RB-3) DNA.
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 sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
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                                                                                                                                                                                      Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;
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Matches 1042; Conservative
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/\*tag= a /product= ' Yeh ..1732 Medlock E, 2002-055100/07. (AMGE-) AMGEN INC. P-PSDB; AAM47458 WO200168705-A2 Homo sapiens 20-SEP-2001 Jing S, Key 2198 2258 1447 2318 2378 2438 1627 2498 2558 1747 1387 1507 1687 GAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAA 2678 GGAAAAAGCCTGCCACGATGGTGCTGCTCTTGTAGCCCACCATGAGAAG GCCAAGAGCGAGGCCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAAC GCCAAGAGCGAGGCAGTCCCAGTGAGACTCTCAAGACCTCTTCCCCCTTGCCTTTAAC AGAGAGATTGATACAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTC CAAGAGACCTTAAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAAACGTGTGATGATCCT CAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCT CAGAAAAAAAAAATAGCAGAGAGATGGGTCCAGTGCAGTGCCTTGCCACTCAAAAGAAGGCA GCAGACAAAGTCGTCTTCCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGT GCAGACAAAGTCGTCTTCCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGT CTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAAATACGTGGTGTCTACTTT **AGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACTTC ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGGTGTCAGCA** CTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTT

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The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye; tumour; ss.
                                                                                                                                                                                                                                                                                   1987
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diagnosing, ameliorating or
(e.g. psoriatic arthritis) and
                                                                                                 TITICAAATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACT
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12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0723232.
02-FEB-2001; 2001US-266159P.
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disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischaemia), eye disorders, reproductive disorders, tumours and
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Pred. No. 1.2e-236;
0; Mismatches 3; Indels
                                                                               Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;
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Local Similarity 99.7%;
les 1042; Conservative (
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Matches 1042;
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                                          TCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACTGTAACCATTTT
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Pred. No. 1.7e-236;
0; Mismatches 9; Indels 0;
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, Zhang J, Werhman T;
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                                                                               GATAATGCAACAATAAAGCATCTTC
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P-PSDB; AAM24349.
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03-AUG-2000;
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ACAAAAGCAAGCGGGA 871 GGGTGCTGGTGGCAGGG 1958 [			AAACTACATTTACAACT 2738 
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812 1899 872 1959 932 2019	2079 1052 2139 11112 2199 1172 2259 1232 2319 1232	2379 1352 2439 1412 2499 1472 2559 1532 2619	2679 1652 2739 1712 2799 1772
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Search completed: May 28, 2003, 00:09:08 Job time : 782.385 secs

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May 27, 2003, 22:37:09; Search time 7273.44 Seconds (without alignments) 11427.544 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	Description	AF208111	AC113172	AC012467	AF208110	AX061651	AX350967	AA233209 AX253204	AX365258	AX253207	AX365260	BC000980	AF212365	AF250309		AX180774	AX376332	AX350969 Seque	AFZUBIUB BC026546	AF208109 Mus	AC093357 Mus m	AX07169	625993 629993	AX098181 Sequence	AX35097		AC11726	AC11708	AX25201	AX45855	AX34453	AX34524	AC11591	AX34555	AC116988 Dictyos	AX345452 Sequenc	AAS48334 Sequence 277 AC034277 Homo sapi	ALIGNMENTS		56 bp mRNA linear PRI 17-JUL-2000 17 receptor homolog precursor (EVI27)			ca, Craniata, Vertebrata, Buteleostomi, es: Catarrhini: Hominidae: Homo.	
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/ Jacks transmembrane and cytoplasmic domains"
/ Codon start=1
/ Codon start=1
/ Product="truncated IL-17 receptor homolog precursor"
/ Protein id="Aph86052.1"
/ Ab_xref="G1:9246435"
/ Ab_xref="G1:9244435"
/ Ab_xref="G1:92444455"
/ Ab_xref="G1:92444455"
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3 2 (bases 1 to 2856)
S Shaughnessy,J.D. Jr.
Direct Submission
AL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St, Little Rock, AR 72212, USA
Location/Qualifiers
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   encodes a novel membrane protein with homology to the IL17
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/gene="EV127"
/product="truncated IL-17 receptor homolog"
204. .206
/gene="EV127"
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/gene="EVI27"
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AC113172 149634·bp DNA linear PRI 31-JUL-2002 Homo sapiens chromosome 3 clone RP11-739J4, complete sequence. . AC113172 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, B.D.
Direct Submission
Direct Submission
Submitted (26-FEB-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases ito 149634)
3 (bases ito 149634)
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. Rouse, G., Wu, Z., Kibukawa, M., Raymond, C. Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 2640 2820 2400 2400 2460 2460 2520 2580 2580 2640 2700 2700 2760 2760 GIGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAA ACGATGCTGCTGCTTGTTGTAGCCCCATGAGAAGCAAGAGACCTTAAAGGCTTCCT GTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGA GCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAAGACG ATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACTTCATGAAGGATGCCACTGCTTTCT ATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACTTCATGAAGGATGCCACTTTCT AACAGCCTTAGTAAATTAAAACATTTTATACCAATAAAATTTTCAAATATTACTAACTAAT GTAGCATTAACTAACGATTGGAAACTACATTTACAACTTCAAAGCTGTTTTATACATAGA AATCAATTACAGCTTTAATTGAAAACTGTAACCATTTTGATAATGCAACAATAAAGCATC GCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACG GTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCC ACGATGGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCT ATCCCACCAATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACA Kaul, R.K., Olson, W.V., Zhou, Y., James, R.A., Saemphimmachak, C., Phelps, K.A., Buckley, D., and Haugen, B.D. Direct Submission Unpublished AC113172.2 GI:22024573 and Haugen, E.D. Direct Submission human. AC113172/c LOCUS SOURCE ORGANISM ' DEFINITION ACCESSION 2401 2581 2641 2641 2281 2341 2341 2401 2461 2521 2761 2821 2821 TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL 2521 2701 2701 REFERENCE AUTHORS 2461 2581 2761 TITLE JOURNAL VERSION KEYWORDS AUTHORS REFERENCE Š g ò g ઠે g ठे q ò g ò g ઠે qq δ g ò g

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/clone lib="RPCI human BAC library 11"
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/note="Single subclone region"
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Pred. No. 1.6e-294;
0; Mismatches 23;
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/note="Single subclone region"
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/organism="Homo sapiens"
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/chromosome="3"
Location/Qualifiers
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Homosapiens Butheria; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Bases I to 17072)

2. (Bases I to 17072)

2. (Bases I to 17072)

3. Bulacy, D.M., Adams, C.C., Balley, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganceb, R., Hernandez, J., Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J., Kodeson, A., Hoques, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Liartz, D., Kelly, S., Kondejewski, N., Kongor, V., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M. P., Melson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Partish, B., Paxton, S., Payton, B., Parton, M., Sparks, A., Stamps, A., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sugang, R., Tabor, P., Taylor, T., Wensford, G., Yu, W., Zhou, X., Nalliamson, A., Welnstock, I. R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nalliamson, A., Nelson, D. and Gibbs, R. Direct Submission

1. Opposite the state of 177072 bp DNA linear PRI 15-WAR-2002 Homo sapiens chr3 BAC RPI1-884K10 (Roswell Park Cancer Institute AC012467 Submitted (28-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 137015 1443 GAAGCCAAGAGGATCACTGCTGCTCCTTTTTGTAGAGGAAATGTTTGTGTGTACGTGGTAA 1502 Db 136774 TGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAACAAGAGGGGTC Db 137014 GGTTCAGACCCCGGGAGTCTTGGGCACGTGGGTCTCGGGTCACTGGTTTTGACTTTAGGG Db. 136954 CTTTGTTACAGATGTGTGTGAGGGAAAATGTGCATGACAACAACATGAGAGGTATGGGCG DD 136834 GCATGGTGTGAACTTTCTGAGCCTCTTGTTTTTCCTCAGCTGACTCCATATTTTCCTACT TGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTC gaagccaagaggarcacrgcrgcrccrrrrrrrrrrgagggaaargrrrgrcracgrggraa Db 137074 GATATGACCTAGCCCTTTTAGGTAAGCGAACTGGTATGTTAGTAACGTGTACAAAGTTTA CTTTGTTACAGATGTGACCAAGGGGAAAATGTGCATGACAACACTAGAGGTAGGGGCG <u>AAGCCAGAAAGAAGGGAAGTTTTGGCTGAAGTAGGAGTCTTGGTGAGATTTTTGCTGTGAT</u> AAGCCAGAAAGAAGGAAGTTTTGGCTGAAGTAGGAGTCTTGGTGGAGATTTTGCTCTGAT GCATGGTGTGAACTTTCTGAGCCTCTTGTTTTTCCTCAGCTGACTCCATATTTTCCTACT gerrcagaccccgggagrcrrgggcargrgggrcrcgggrcacrggrrrrgacrrraagg Db 136714 CCTTTCCCTCTGGATAACAGTAAGTGC 136688 CCTTTCCCTCTGGATAACAAAAGC 1889 AC012467.9 GI:7363385 (bases 1 to 177072) Direct Submission Homo sapiens. Homo sapiens Worley, K. RESULT 3 AC012467/c LOCUS VERSION KEYWORDS SOURCE ORGANISM DEFINITION AUTHORS TITLE JOURNAL Db 136894 Qy 1863 JOURNAL REFERENCE 1563 1683 1803 Db 137134 1743 ACCESSION 1503 1623 REFERENCE AUTHORS ઠ à à ð ð ò ò

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gataggactt (c) cagtacaata
gggcttgaac (a) aacgaatgcc
cactcagaag (t) ggtttcatgc
actttaatta (g) atcttttgaa
tttaattaga (t) cttttgaaat
gaggatocto (a) ogatgaacat
tototoatto (c) taagttacot
caagcottot (c) ttttoagata
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'db_xref="taxon:9606"
'chromosome="3"
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complement(5146. .5401)
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/rpt_family="MER4C"
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628. .2901
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complement (3408. .4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Muc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Peports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                      Direct Submission
Submitted (15-WAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
OM Max 31, 2000 His sequence version replaced gi:7144718.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                    Department
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aaaaaaaa (a) cctagacaga
tgtgggggg (t) actatacat
tcccttctgg (t) gcttttttc
                                Direct Submission
Submitted (31-MAR-2000) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
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(bases 1 to 177072)
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5197. .5473
/standard name="DM1-4H8A/DM1-4H8B"
/db xref="dbST8:52070"
5402. .5427
                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                Score 1178.8; DB 9
Pred. No. 1.6e-294;
0; Mismatches 23;
                                            5402. .5427
/rpt family="(TTA)n"
complement (5428. .5717)
/rpt family="Aludb"
complement (5718. .5777)
/rpt family="LiMB6"
complement (5718. .5777)
/rpt family="LiMB6"
complement (578. .6082)
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/rpt family="LiMB6"
complement (6083. .7264)
/rpt family="LiMB6"
complement (7265. .7437)
/rpt family="FAM"
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Best Local Similarity 98.0%;
Matches 1203; Conservative
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1828 bp mRNA linear PRI 17-JUL-2000 complete cds.
AF208110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1828)
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1. .1821
formap="EV127"
/mote="linked to ecotropic viral integration site 27 in myeloid leukemias"
6. .1514
/gene="EV127"
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Shaughnessy, J.D. Jr.
Direct Submission
Submitted (24.NOV-1999) Myeloma and Transplantation Research
Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St, Little Rock, AR 72212, USA
                                                                                                                                                          57596 GGITCAGACCCCGGGGAGICTTGGGCACGTGGGTCTCGGGTCACTGGTTTTGACTTTAGGG
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                                 57716 GAAGCCAAGGATCACTGCTGCTCCTTTTTTCTAGAGGAAATGTTTGTCTACGTGAA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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/codon_start=1
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LRDRYEPVTTSVATGPYSILMNVSWHADABITELLAGATKICVTGKSNRQSYSCVRC
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GCLDHIMKYKKKCVKAGSLWDPNITACKKNBETVEVNFTTFPLGNRYMALIQHSFIIG
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PPDDNNKSRGGWLPDLLSLLVATWVLVAGTYRMRHERSIKKTSFSTTTLEPPIKV
LVVYPSEICFHHTICYTEFLLGALLVATWVLLSKWQKKKIAEWGPVQWLATQKKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVFRB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="putative GSK3; phosphorylation site"
[643. .1649
|gene="EVI27"
 'product="IL-17 receptor homolog precursor"
                                                                                                                                                                                                                                                                                                                                                                                               GSK3; phosphorylation site"
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                                                                                                                                                                                                                                                                                                               note="putative; glycosylation site"
                                                                                                                                                                                                                                                                      note="putative; glycosylation site"
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Best Local Similarity 100.0%; Pred. No. 1.3e-268;
Matches 1078; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                            product="IL-17 receptor homolog"
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45. .1511
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'gene≂"EVI27"
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/gene="EVI27"
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PAT 24-JAN-2001
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1701)

dumas milne Edwards, J.B., Bougueleret, L. and Jobert, S.

Complementary dna's encoding proteins with signal peptides

Patent: WO 0100806-A 56 04-JAN-2001;

GENSET (FR)
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GCAGACAAAGTCGTCTTCCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGT
                                                                                                                             GGCAAGAGCGAGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAAC
                                                                                                                                                                                                                                                                                                                                              CTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGTCTACTTT
                                                                                                                                                                                                                                                                                                                                                                                 CTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTTTT
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/organism="Homo sapiens"
/organism="tomo: 9606"
/db_xref="taxon: 9606"
/db_xref="taxon: 9606"
/note="unnamed protein product"
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CLDHIMKYKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTIGF
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FLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVVFREI
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1669. .1674
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Pred. No. 1.2e-261;
0; Mismatches 8; Indels
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Best Local Similarity 99.2%;
Matches 1056; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
J. (bases 1 to 1713)
Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and Nguyen, H.O.
Ill Treceptor like molecules and uses thereof Patent: WO 0168705-A 6 20-SEP-2001;
Amgen Inc. (US)
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Pred. No. 8.6e-259;
0; Mismatches 3;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 99.7%;
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/protein_id="CAC93837.1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1841)
Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and NGUyen,H.Q.
11-17 receptor like molecules and uses thereof
Patent: WO 0168705-A 1 20-SEP-2001;
Amgen Inc. (US)
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/organism="Homo sapiens"
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Pred. No. 8.7e-259;
0; Mismatches 3; Indels
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11-17 molecules and uses thereof
Patent: WO 0208285-A 17 31-JAN-2002;
Amgen, Inc. (US)
                         Sequence 17 from Patent W00208285.
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AX36528 GI:18697003
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/db_xref="taxon:9606"
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Best Local Similarity 99.7%;
Matches 1042; Conservative
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2015)
Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and
Ngyven, H.Q.
11-17 receptor like molecules and uses thereof
Patent: WO 0168705-A 4 20-SEP-2001;
Amgen Inc. [US]
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AXX53207.1 GI:15986348
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IDTKDDYNALSVCFKTHMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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Pred, No. 8.8e-259;
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Matches 1042; Conservative
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Pred. No. 8.8e-259;
Mismatches 3; Indels
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11-17 molecules and uses thereof
Patent: WO 0208285-A 19 31-JAN-2002;
Amgen, Inc. (US)
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/organism="Homo sapiens"
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IDTKDDXNALSVCPRYKHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: n Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9246432. Location/Qualifiers
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                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X.,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny, D.M., Gibbs, R.A.
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/tissue_type="Cervix, carcinoma"
/clone lib="NHH MGC_12"
/lab_host="DH10B"
/note="Vector: pCWV-SPORT6"
    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, clone MGC:5245 IMAGE:2985728, mRNA, complete cds.
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ne Inc. (JP); SAGAMI CHEMICAL RESEARCH Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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VFLLSNDVNSVCDGTGCKSEGSPSRNSQDLFPLAFLAFLAFLKVAVVYFRE
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/protein_id="AaP7976.1"
/db xref="GI:870522"
/trānslation="MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDL1PGD
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WYTEAPCTOTGRESGGKWTFSYIGFPUELMTVYFTGAHID INAUNGUEDESMSYNFTSP
GCLDHIMKYKKKCVRASLMPPNITACKKNEETVEVNFTTTPLGNRYMALIOGSENSKYNFTSP
GCLDHIMKYKKKCVRASLMPPNITACKKNEETVEVNFTTTPLGNRYMALIOGSTIG
FSQVFEPHQKKOTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCFQTGV
BPFDDNIKSKPGGWLPLLLSLLVATWYLNAGIYLMRRHERIKKTSFGTTTLLPPIKV
LVVYPSBLCFHTICYFTEFLGNHCRSEVILEKWQKKKIAEMGFVQWLATQKKAAADKV
VFLLSNDVNSVCDGTCGGSEGSPSENSQDSSPCL"
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(bases 1 to 1816)
Shi, Y., Ullrich, S. J., Zhang, J., Connolly, K., Grzegorzewski, K. J., Barber, M. C., Wang, W., Wathen, K., Hodge, V., Fisher, C.L., Olsen, H., Ruben, S. M., Knyazev, I., Cho, Y. H., Kao, V., Wilkinson, K. A., Carrell, J. A. and Bbner, R. A novel cytokine receptor-ligand pair. Identification, molecular Janace rization, and in vivo immunomodulatory activity
J. Biol. Chem. 275 (25), 19167-19176 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-DEC-1999) Molecular Biology, Human Genome Sciences,
Inc., 9410 Key West Avenue, Rockville, MD 20850, USA
Location/Qualifiers
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CAAGAGACCTTAAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCT
                                         GAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAA
                                                                              TTTTCAAATATTACTAACTAATGTAGCATTAACTAACGATTGGAAACTACATTTACAACT
                                                                                             1670 TTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACGAAACATTAACAACT
                         GAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAATAAAA
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Homo sapiens IL-17B receptor (IL17BR) mRNA, complete cds
AP212365
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Pred. No. 1.3e-256;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.1"
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                                        1583 bp mRNA linear PRI 17-APR-2001
Homo sapiens putative cytokine receptor CRL4 precusor mRNA,
Complete cds.
AP250309
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VFLLSNDVNSVCDGTCGKSEGSPSENSQDLPPLAFNLFCSDLRSQIHLHKYVVYYFRE
IDTADYNALSVCPRYKMOATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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GCLDHIMKYKKKCVKAGSLMDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTIIG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1583)

Zhang, W. and Cao, X.

Direct Submissers

Submitted (29-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,

800 Xiangyin Rd., Shanghai 200433, P.R. China
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1. 1509
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BM693867 UI-E-DWI-AV727345 AV727345 AV727345 AV727345 AV727345 AV727345 B1458542 603198643 B162184 G102184 G10
BI823321 603041231
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM11116 row: 1 column: 19
High quality sequence start: 4
High quality sequence stop: 768.
Location/Qualifiers
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BB653710 BB653710
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BB307800 BB307800
BB644125 BB644125
AL535617 AL535617
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11663.832 Million cell updates/sec
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Copyright (c) 1993 - 2003
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/clone="INAGE:5042466"
/clone=lib="NCI CGAP_Kid14"
/lab host="Hol10B (T1 phage-resistant)"
/lab host="lorgan: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/lab host="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/lab host="In thing to the transport of transpo
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RESULT 2 BB653710

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Ta (bases 1 to 710)

Rakawa,T., Carninci,F., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suro,H., Riken Mouse ESTS (Arakawa,T., et al. 2001)

Unpublished (2001) Contractory for Genome Exploration Research Group, RIKEN Genomic Exploration Ferlia (1970). Yokohama Institute Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of F Pratiature of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Email: genome-resegescriken.go.jp, URL:http://genome-resegescriken.go.jp, URL:http://genome-gsc.riken.go.jp, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh, W., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y. Normalization and subtraction of Gap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 167-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ;S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGGGCGCAACTCGAGTTTTTTTTTTTTVN 3'], cDNA was EST 26-OCT-2001 /clone\_lib="RIKEN full-length enriched, adult male liver. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. RIKEN full-length enriched, adult male liver tumor Mus cDNA clone C730019M05 5', mRNA sequence. **MRNA** tissue type="liver tumor" /dev stage="adult" /lab\_host="DH10B" BB653710 RIKEN full-length enrich musculus cDNA clone C730019M05 5' organism="Mus musculus" 710 bp /db\_xref="taxon:10090" /clone="C730019M05" Location/Qualifiers BB653710.1 GI:16487538 /sex="male"

GI:16398958

BB667509.1

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ORGANISM
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34.0%; Score 668.4; DB 10
Best Local Similarity 99.1%; Pred. No. 3.1e-124;
Matches 694; Conservative 0; Mismatches 1;
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ORIGIN
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EST 24-0CT-2001

728 bp mRNA linear EST 24-OCT-: BB667509 RIKEN full-length enriched, adult male liver tumor Mus musculus cDNA clone C730019M05 3', mRNA sequence. BB667509

DEFINITION

RESULT 3 BB667509 LOCUS ACCESSION

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Email: genome-resegac.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

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Hayashizaki,Y.

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Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

Hayashizaki,Y.

Rick, Hara,A., Itoh,M., Kawai,J., Shibata,K. and

Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

Hayashizaki,Y.

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Rick, Hara,A., Itoh,M., Kawai,J., Shibata,K. and

'K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and

'K., Rick, Shibata, K. and

'K., Rick,
                                                                                                    1 (bases 1 to 728)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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'clone="C730019M05"
'clone=lib="RIKEN full-length enriched, adult male liver
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue type="liver tumor"
dev stage="adult"
lab_host="DH10B"
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/organism="Mus musculus"
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           was cleaved with BamHI and KhoI. Vector: a modified Baluescript KS(4) after bulk excision from Lambda FLC I. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistence we gratefully acknowledge.
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0; Mismatches 14;
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Best Local Similarity 97.5%;
Matches 658; Conservative
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EST 31-AUG-2001

BB307800
BB307800 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus CDNA clone B230216H15 3', mRNA sequence.

BB307800.2 GI:15411368

Mus musculus house mouse

EST.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

BB307800

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Rayashizaki, Y.

Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)

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Func. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                        Mammalia, burneria; Rodentia; Scilloghanii; Muridae; Mulliae; Mus.

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kouno,H., Kouda

,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki
,Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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 Muramatsu,M. and Hayashizaki,Y. et al. 2001)

IL Unpublished (2001)

On Jul 10, 2000 this sequence version replaced gi:9008505.

Contact: Yoshihide Hayashizaki
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  The Institute of Physical and Chemical Research (RIKEN)

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  Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Komno,H., Okazaki,Y., Miramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Arakwa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
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URL:http://genome_ggsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Gyazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak., D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/sex="male"
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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/db_xref="taxon:9606"
/clone="CSODF016YG03"
/clone lib="LTI FL013 FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
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Homo sapiens cDNA clone CSODF016YG03 5
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I, Nassa I to 869)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                    GTGGCCAGTGGCCGGCCCATGTTGCTAGTGTTGCTGATCTTGGCTGCTGCTGCAGCGCCAGGCCAGCAGCAGCAGCTGGTTGCTAGTGTTGCTGATCTTGGCTGCTGCTGCTGCAGCAGC
                                                                                         GCCCTGCCTCGAGAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGG
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pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com"
/note="Organ: Fetal brain; Vector: pCMVSFORT 6; 1st strand chapter by primed with a Not!-Oilgo(df) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the
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; Pred. No. 4.2e-92;
17; Mismatches 175;
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BF322373 431 bp mRNA linear EST 21-NOV-2000 maa24a07.x1 NCI_CGAP_Li10 Mus musculus cDNA clone IMAGE:3811861 3', mRNA sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 431)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
CTTGTTGAAGGCCACCAAGATTTGTGTGTGACGGCCAAAAGCAACTTCCAGTCCTACAGCTG
                                                                     TGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCTTCCGGCGGCAAATG
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
//note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
Oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
                                                                                                                                                    BI823321 946 bp mRNA linear EST 04-OCT-2001
60341231F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11454 row: m column: 08
High quality sequence stop: 795.
Location/Qualifiers

1. 946
                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosto Bukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 946) NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 GCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGTCCAACACAC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TCTAATCCCGGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 456.8; DB 13; Length 946;
Pred. No. 8.5e-82;
0; Mismatches 202; Indels 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182255"
/clone="lib="NIH"MGC_115"
/-t___=="main.org"
    865
                         CCATCCCTCCAGATGACACAGACGCA
                                                                                                                                                                                                                          BI823321.1 GI:15934871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.3%;
Best Local Similarity 72.9%;
Matches 710; Conservative
                                                                                                                                                                                                       mRNA sequence.
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                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                           DEFINITION
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  839
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AUTHORS
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                                                                                                               RESULT 7
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1 (bases 1 to 425)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3/); double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and choned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two Younds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1306 GATTTCAGCAGCCAGACGCATCTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGAC 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAA 1545
                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAAAGGCGACTATAATGCCCTGAGTGTCTGCCCCCAATATCATCATCATGAAGGACGCC 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1426 ACAGCTTTCCACACAGAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCA 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTTCCTACTCTCCCTTCCAGTGACAAATGCTGTGACGACTCTGAAATGTGTGGGAG 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGCTITCCACACAGAACTICTCAAGGCTACGCAGAGCATGTCAGTGAAGAACGCTCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CAAGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAA
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                                                                                                                                 Waterston, R. The Wash Unuse EST Project The Wash-HMM Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project Wash-HMM Mouse EST Porject Park 214 286 1800
Feb.: 314 286 1810
Feb.: 314 286 1810
Feb.: 314 286 1810
Feb.: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:1345453"
/clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 402. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 423.4; DB 9,
Pred. No. 5.3e-75;
0; Mismatches 1;

    .425
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
21.6%;
Best Local Similarity 99.8%;
Matches 424; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                          MGI:694245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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ORIGIN
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JOURNAL
COMMENT
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                         REFERENCE
                                              AUTHORS
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                       DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                         /dev_stage="10 weeks"
/lab host="nH10B (T1 phage-resistant)"
/hote="Organ: liver; Vector: pCMV-SPORTs, Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Sybradge innert size 1.6 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1196 TICCCAGIGACGICCCGACCCITIGIGACAGIGCCTGIGGCCACAAIGAGGGCAGCGCCA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAGAACTCTCAGGATCTGTTCCCTCTTGCCTTTTAACCTCTTTTGTAGTGATTTCAGCA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGACGCATCTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGCACCTCAAAGGCG 1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCCCTTCCAGTGACAAATGCTGTGACGACTCTGAAATGTGTGGGAGGGCTGTGTG 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 TTCCCAGTGACGTCCCGACCCTTTGTGACAGTGCCTGTGGCCCACAATGAGGGCACGCCCA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252
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  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 GGGAGAACTCTCAGGATCTGTTCCCTCTTGCCTTTAACCTCTTTTGTAGTGATTTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ACTATABATGCCCTGAGTGTCTGCCCCCAATATCATCTGTGAAGGACGCCACAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 GCCAGACGCATCTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAAGGCG
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.0%; Score 431; DB 12; Best Local Similarity 100.0%; Pred. No. 1.6e-76; Matches 431; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         1. .431
/organism="Mus musculus"
/db xxef="taxon:10090"
/clone="IMAGE:3811861"
/clone lib="NCI_CGAP_Lil0"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 t
                                                                                                                                                      Seq primer: -40UP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
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AV709899
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1 (bases I to 703)

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6 (bases I, to 703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zeguang Hann
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
191: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
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                                                                                                                                           TGTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCCAGACCCTCTGGTGGTAAA
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Pred. No. 1.5e-67;
0; Mismatches 151; Indels
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This clone is available at CHGC in Shanghai.
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/clone="ADCACB04"
/clone lib="ADC"
/tissue_type="Adrenal gland",
/dev stage="Adrenal gland",
/lab_host="SOLR"
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/organism="Homo sapiens"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mational to 561)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: bb40e05.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs: romail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Prazayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

image.llnl.gov/mage/Hhml/iresources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                      AW675096 561 bp mRNA linear EST 11-APR-2000 bb40e05.yl NIH MGC 12 Homo sapiens cDNA clone IMAGE:2985728 5' similar to TR:043844 043844 IL-17 RECEPTOR. ;, mRNA sequence.
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/clone="IMAGE:2985728"
/clone=lb="NIH MGC 12"
/tissue_type="cervical carcinoma cell line"
/lab host="Pull MGC 12"
/lab host="lab" (Anote 10 Cone 11 C
1666 ACCTGAGCATACACGCCTGAGGCTAGTCATTGGCTGGATTTATGAAGACAACACAGTTAC 1725
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                                                          361 ACCTGAGCATACACGCCTGAGGCTAGTCATTGGCTGGATTTATGAAGACAACAGTTAC
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Pred. No. 5.2e-70;
0; Mismatches 102; Indels 0;
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AW675096
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AUTHORS
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1. :551
/ Organism="Sus scrofa"
/ db xaref="teaxon.9823"
/ clone_lib="MARC 1PIG"
/ tissuue_type="pooled"
/ lab host="#UHOB"
/ note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
3 138 c 150 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTGCCTCGAGAGCCGACTATTCAGTGTGTGTTGAGACAGGGCCATCTCCAGAGTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGTCCAACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGGCGGCGAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGGCGCCAAATGGATGTTTTCCTACGTAGGCTTTCCAGTAGAGCTGAATACACGCTAT 428
                                                                                                                                                                                                                                                                                                                                                                                 9 écedesadriceccecedanterractadrecrecredecerecedecreredeser 68
                                                                                                                                                                                                                                                                                                                                                    GTGGCCAGTGGCCGGGCCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ACAAGTGTGGCAGCAGCAGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGTGTTGCAGTGGAGGACTATTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 551;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                               Score 381.4; DB 12;
Pred. No. 1.3e-66;
0; Mismatches 101;
                     Plate: 91 row: J column: 1
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
     BACKWARD: GITITCCCAGICACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI360842.1 GI:15056870
                                                                                                                                                                                                                                                                            19.4%; initarity 81.4%; Conservative 0;
                                                                                                                                                                                                                                                                                                 Similarity
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1. (bases 1 to 551)

1. (bases 1 to 551)

1. (bases 1 to 551)

1. Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

1. Unpublished (2000)

1. Contact: Smith TPL

1. USDA, ARS, US Meat Animal Research Center

1. PO Box 166, Clay Center, NE 68933-0166, USA

1. Tel: 402 762 4396

1. Fax: 402 762 4396

1. Email: smith@email.marc.usda.gov

2. Single pass sequencing. Bases called and alt trimmed with phred vo.980904.e. Vector identified by cross_match with the -minscore 18 and -minmarch 12 options.
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                     121
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302 GACAGTAGAAGTGAACTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCA
                                                                                                                                                                                                                                                                                                                                  ACGGGACACGACATTGGGGTTTTCTAGAGTGCTGG------AGAATAAACTGATGAG
                                                                                                                                                                                                                                                                                                                                                                  362 ACACAGCACTATCATCGGGTTTTTCTCAGGTGTTTGAGCCCACACCGGGAGGAACAACGCG
                                                                           474 TITGICTGTGAACTICACCICGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCA
                                                                                                                                          182 CATGTCTGTGAATTTCACCTCACCCGGCTGCCTAGACCACATAATGAAATATAAAAAAA
                                                                                                                                                                                                             GATGGTTGAAGTGAATTTCACAACCCATCCCCTTGGAAACAGATACAGATTCTCATTCA
                                                                                                                                                                                                                                                                                                                                                                                                      GACGTCTGTAGCCATCCCGGTGACTGAGGAGAGAGGTGCGGTGGTTCAGCTGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       422 AGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTTTTCCTACTTGCACGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAAACAGGCGTNCCTTTTCCTCTGGATAACAACAAAGCAAGCCGGGAGGCTTGGCTGC
                                                  GTGCACTGAGGCGGGAAGCCTGTGGGACCCCAGACATCACTGCTTGTAAAAAGAACGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTTACATACCTGCGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG384365 551 bp mRNA linear 303426 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG384365 GI:13308837 EST.
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGAGGCAAG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGATGCACG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pig.
Sus scrofa
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KEYWORDS
SOURCE
ORGANISM
                  62
                                                    414
                                                                                  122
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248

368

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EST 01-AUG-2001
                                                                                                                                         pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 588)
588 bp mRNA linear
388904 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence
BI360842
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AAS 62342 370 bp mRNA linear EST 18-AUG-1997
V122h03.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone
ARGES 973013 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 370)
Marram, Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1586 GACTCTGAAATGTGTGGGAGAGGCTGTGTGGAGGTAGTGCTATGTACAAACTTGCTTTAA 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1646 AACTGGAGTTTGCAAAGTCAACCTGAGCATACACGCCTGAGGCTAGTCATTGGCTGGATT 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1766 AGCTGGGTAATGATTATCACTGAGAACCACGCACTCTGGCCATGAAGTAATACGGCACTT 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACTCTGAAATGTGTGGGAGGCTGTGTGGGAGGTAGTGCTATGTACAAACTTGCTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGGAGTTTGCAAAGTCAACCTGAGCATACACGCCTGAGGCTAGTCATTGGCTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 366.8; DB 9; Length 370;
Pred. No. 1.3e-63;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:973013"
/clone_lib="Stratagene mouse Tcell 937311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector to vector length is 377
Seg primer: -28mil zevl ET from Amersham
High quality sequence stop: 326.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
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                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                       house mouse
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AA562342
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 G.A., Smith, T.P.L., Casas, E.,
Bennett, G.A., Laegreid, W.W.
                                                 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /notē="Vector: pCMV SPORT6; Site 1: Not1; Site_2: Sal1; Libraty made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennet and Keele,J.W.
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/db_xref="taxon:9823"
/clone_lib="WARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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//dev stage="adult"
/lab.host="bluelle"
/lab.lowing tissue(s): lens. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dr primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (d7)18 tail. The
sequence tag for this library is CGATTAGGGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
761: 319 335 8250
Fax: 319 335 9565
Email: meocares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seg primer: MJ Reverse.
                                                                                                                                                                                                                                                                                                                   UI-E-DW1-ahe-i-22-0-UI.rl UI-E-DW1 Homo sapiens CDNA clone UI-E-DW1-ahe-i-22-0-UI.rl UI-E-DW1 Homo sapiens CDNA clone BM693867 BM693867.1 GI:19007125
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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181 AGCTGGGTAATGATTATCACTGAGAACCACGCACTCTGGCCATGAGGTAATACGGCACTT
                                                                                                 241 CCCTGTCAGGCTGTCTGTCAGGTTGGGTCTGTCTTGCACTGCCCATGCTCTATGCTGCTGC
                                                                                                                                       GTAGACCGTTTTGTAACATTTTAATCTGTTAATGAATAATCCGTTTGGGAAGCTCTCAAA
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/db xref="taxon:9606"
clone="UI-E-DW1-ahe-i-22-0-UI"
/clone_lib="UI-E-DW1"
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Score 366; DB 14;
Pred. No. 1.6e-63;
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Sequence 11, A
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Sequence 3, Application US/09778971

Sequence 3, Application US/09778971

Sequence 3, Application US/09778971

SERENT NO. US20020102639A1

GENERAL INFORMATION:

TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby

TITLE REFRENCE: D6138

CURRENT APPLICATION NUMBER: US/09/778,971

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/180,374

PRIOR PILING DATE: 2000-02-04

SEQ ID NO 3

SEQ ID NO 3
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; OTHER INFORMATION: cDNA of mouse Evi27
US-09-778-971-3
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Matches 1963; Conservative
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ORGANISM: Unknown
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Oy       241 GACGCCAGCATCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATG       300         Db       241 GACGCCAGCATCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATG       300	OY 301 AATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCT 360	Oy 361 TCCGGCGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTAT 420 Db 361 TCCGGCGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGGACTCTTAT 420	Qy       421       CTCATCAGCGCCCATAACATCCCCAATGCTAATGAGGACAGCCCTTCTTTGTCT       480         Db       421       CTCATCAGCGCCCATAACATCCCCAATGCTAATGAAGGACAGCCCTTCTTTGTCT       480	Oy 481 GTGAACTTCACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACT 540 Db 481 GTGAACTTCACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACT 540	OY 541 GAGGCGGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTT 600 	OY 601 GAAGTGAATTTCACAACCCATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGAC 660 	Qy       661       ACGACATTGGGGTTTTCTAGAGTGCTGGAGAATAAACTGGATGAGGACGTCTGTAGCCATC       720         Db       661       ACGACATTGGGGTTTTCTAGAGTGCTGGAGAATAAACTGATGAGGACGTCTGTAGCCATC       720	Qy       721       CCGGTGACTGAGGAGTGAAGGTGGGTTCAGCTGACCCCCATATTTACATACCTGC       780         Db       721       CCGGTGACTGAGGAGGTGCAGGTTCAGCTGACCCCATATTTACATACCTGC       780	OY 781 GGCAATGACTGCATCGGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGCTCCC 840	OY 841 ATCCTCCAGATGACAGACGCTGCTGGGAGGCTGGCTCTCTTCCTGGTGCTG 900	Oy 901 CTGGTGGCTGTGGGGGGGGGGGGGGATCTACCTAACTTGGAGGAAGGA	y 961 ACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTCACTTAAGGTCCTGGTGGTT 1020	y 1021 TATCCTTCTGAGATATGTTTCCATCACCGTCTGTCGCTTCACTGACTTTCTTCAAAC 1080 	Y 1081 TACTGCAGAAGTGAGGTCATCCTTGAAAAATGGCAGAAAAGAAAATCGCCGAGATGGGG 1140 	y 1141 CCGGTACAGTGGCTGACCACTCAGAAGCAAGCAGATAAAGTGGTCTTCCTTC	y 1201 AGTGACGTCCCGACCCTTTGTGACAGTGCCTGTGGCCACAATGAGGCAGGC	y 1261 AACTCTCAGGATCTGTTCCTCTTGCCTTTAACCTCTTTTGTAGTGATTTCAGCAGGCAG	Y 1321 ACGCATCTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAAGGCGACTAT 1380
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Evi27 Gene Sequence and Protein Encoded Thereby
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TION NUMBER: US/09/778,971
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Patent No. US20020037524A1

GENERAL INFORMATION:

APPLICANT: Wedlock, Eugene
APPLICANT: Scott M.
APPLICANT: Billoc, Gard
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APPLICANT: Dilac, Gard
APPLICANT: Dilac, Gard
APPLICANT: Jing, Shuqian
TITLE OF INVENTION: Like Molecules and Uses Then
TITLE OF INVENTION: 11-17 Like Molecules and Uses Then
FILE REPERENCE: 01017/37128B
CURRENT APPLICATION NUMBER: US/09/886,404

CURRENT FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-06

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-06-21

PRIOR FILING DATE: 2000-06-21

SPRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

SOFTWARE: PATENTIN NUMBER: 60/213,125

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN Ver. 2.0
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APPLICANT: Gorman, Daniel M.

TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
LENGTH: 1796
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LOCATION: (1).. (1509)

OTHER INFORMATION:

NAME/KEY: mat_peptide

LOCATION: (46)..()

OTHER INFORMATION:

US-09-863-8180-1
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ORGANISM: Homo sapiens
FEATURE:
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NAMENKEY: prim transcript

OTHER INFORMATION: cDNA of human Evi27
US-09-778-971-1
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Patent No. US20020102639A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
FILE REFERENCE: D6138

CURRENT APPLICATION NUMBER: US/09/778,971

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/180,374

PRIOR PILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SEQ ID NO: 9
1378 GCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAA
                                                                                                                                                                                                              62 GCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGA
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                                                                     CTTCTCAAGGCTACGCAGGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGATAGC
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Pred. No. 0;
); Mismatches 337;
                                                                                                                                                                                                                                                                                               1562 TTCCAGTGACAAATGCTGTGACGACTCTGAA 1594
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APPLICANT: Yangura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P138 HISTOLIP3 (US)
CURRENT APPLICATION UNMBER: US/09/874,503
CURRENT FILING DATE: 2001-06-05
1499 CTGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAAGGCTTCCTATCCCAC 1558
                                                                                                                         CAATTACAGGGAAAAACGTGTGATGATCCTGAA 1592
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PRIOR PELILANG DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 60/244,072
PRIOR FILING DATE: 2000-10-26
PRIOR PELICATION NUMBER: US 60/242,837
PRIOR PELICATION NUMBER: US 60/175,481
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-06-22
PRIOR PELING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/131,807
PRIOR PELING DATE: 1999-12-23
PRIOR PELING DATE: 1999-12-23
PRIOR PELING DATE: 1999-06-19
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 60/131,022
PRIOR PELING DATE: 1999-06-19
PRIOR PELING DATE: 1999-06-19
PRIOR PELING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/131,022
PRIOR PELING DATE: 1999-06-12
PRIOR PELING DATE: 1999-06-12
PRIOR PELING DATE: 1998-05-14
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1998-12-23
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PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-16
PRIOR PELING DATE: 1998-05-15
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PRIOR PELING DATE: 1908-05-15
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FILING DATE: 2000-12-20
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APPLICATION NUMBER: US 09/380,138
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Patent No. US20020177188A1
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Gurney, Austin L.
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Hillan,Kenneth J.
Hymowitz,Sarah G.
Tumas,Daniel
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Vandlen, Richard
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Williams, P.Mickey
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                   INFORMATION
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                                                                                                                                                                                                                RESULT 6
US-09-874-503-11
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          ACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACATTGGGG
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Pred. No. 3e-313;
0; Mismatches 309;
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR APPLICATION NUMBER: US PCT/USO1/06520
PRIOR APPLICATION NUMBER: US PCT/USO1/06520
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-12-01
PRIOR PLING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/USO0/33673
PRIOR APPLICATION NUMBER: US PCT/USO0/330873
PRIOR APPLICATION NUMBER: US PCT/USO0/3328
PRIOR PILING DATE: 2000-11-10
PRIOR PILING DATE: 2000-08-24
PRIOR PLING DATE: 2000-08-24
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US PCT/USO0/05841
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
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PRIOR FILING DATE: 1999-03-08
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Best Local Similarity 78.7%;
Matches 1194; Conservative
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URRENT APPLICATION NUMBER: US/10/000,157
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PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/130232
PRIOR APPLICATION NUMBER: 60/131022
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-06-36-14
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-10-11
PRIOR APPLICATION NUMBER: 60/13607
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/24837
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/243807
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PRIOR APPLICATION NUMBER: 60/24448
PRIOR PILING DATE: 2000-10-29
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PRIOR PILING DATE: 2000-08-22
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                                                                                        APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddwark, Paul L.
APPLICANT: Grimaldi, J.Christopher
APPLICANT: Gurney, Austin
Sequence 11, Application US/10000157
Publication No. US20020182673A1
GENERAL INFORMATION:
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FILING DATE: 2001-07-18
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VanLookeren, Menno
Vandlen, Richard
Matanabe, Colin
Williams, P. Mickey
Wood, William
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illan, Kenneth J.
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Tumas, Daniel
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PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 1999-03-08
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PRIOR FILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-03-02
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Best Local Similarity 78.7
Matches 1194; Conservative
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APPLICANT: Eaton, Dan L.
APPLICANT: Flivarceff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godward, Audrey
APPLICANT: Godward, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
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78.7%; Pred. No. 3e-313;
iive 0; Mismatches 309;
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 157, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
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Best Local Similarity 78.7
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RESULT

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APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REPERENCE: P1381HACIP1 (US)
CURRENT APPLICATION NUMBER: US/09/747, 259
CURRENT FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cceccearcrecrescrecrecrasecrescescescrerecases es 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 3e-313;
0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DS 00/1/2,036
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 2000-01-11
PRIOR PRINCH DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR PELING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR PELING DATE: 2000-03-12
PRIOR PELING DATE: 2000-03-13
PRIOR PELING DATE: 2000-03-13
PRIOR PELING DATE: 2000-03-13
PRIOR PELING DATE: 2000-03-13
PRIOR PELING DATE: 2000-06-12
PRIOR PELING DATE: 2000-06-12
PRIOR PELING DATE: 2000-06-22
PRIOR PELING DATE: 2000-06-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-10
PRIOR PELING DATE: 2000-11-10
PRIOR PELING DATE: 2000-11-10
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
Dication US/09747259
US20030008815A1
                                                                                                                                                                                                                                                                                     Grimaldi,Christopher
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Best Local Similarity 78.7%;
Matches 1194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, P.Mickey
                                                                                                                             Chen, Jian
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vandlen, Richard
                                                                                                                                                                                                                                                                                                                                               Li,Hanzhong
Hillan,Kenneth
                                                                                                                                                                                                                       Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe,Colin
                                                                                             APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                              Gurney, Austin
                                                                                                                                                                                                                                                    Godowski, Paul
                                                                                                                                                                                       Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood,William
Sequence 11, Application
Publication No. US2003000
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CORGANISM: Homo Sapien
US-09-747-259-11
                                                         GENERAL INFORMATION
                                                                                                                                                                                                                       APPLICANT
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3; SCCAGGGAG 1260 |||| ||| ||| |CCAGTGAG 1257 AGCAGCCAG 1320 || || || || || AGAAGCCAG 1317 3GCGACTAT 1380 | || | || || 3ACGATTAC 1377 GCCATGAT 1500 |||| |||| |GCCACGAT 1497 TTCTTTCC 1197 AND NUCLEIC STCCAACAC 132 | ||||| |TACAACAT 120 AGTGTGGCA 192 ||||| ||| AGTGTTGCA 180 TIGCCTCGA 72 | || || || || TIACCCCGA 60 CAGCATC 252 15; Gaps 1515;

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AACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAG 1317
                                                                                                                                                                                                                                                                                                                                    GAACTTCTCCATGTCAAGCAGCAGCAGTGTCAGCAGAAAAAGATCACAAGCCTGCCACGAT 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GATCTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTTGTTGAAGGCCACCAAGATCTGCGTGAGGGCAAAAACAACATGAATTCATACAGC 312
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                                                           ATTCATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTGATACAAAAGACGATTAC
                                                                                                                                                                        AATGCCCTGAGTGTCTGCCCCCCAATATCATCTCATGAAGGACGCCACAGCTTTCCACACA
                                                                                                                                                                                                                           Aariscreteksigiereriseeseksigieren aariscreteksigieren aariscreteks
                                                                                                                                                                                                                                                                                 GAACTICTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGAT
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APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Chang, Camin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBURCE: P3430RIC104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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Pred. No. 3e-313;
0; Mismatches 309;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-176-758-399
US-10-176-758-399
Sequence 339, Application US/10176758
Publication No. US20030008353A1
SENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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                                                                                                                                                                                                                                                                                                                                                                                          AGCTGTTCACCCTTGTAG 1518
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 78.7
Matches 1194; Conservative
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ORGANISM: Homo Sapien
US-10-176-758-399
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1138 CCAGTGCAGTGCCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTTCC 1197
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181 ACAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATC
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Sequence 157, Application US/10063616

Sequence 157, Application US/10063616

Publication No. US20030013855A1

GENERAL INFORMATION:

APPLICANT: Eston, ban L.

APPLICANT: Godwaf, Audrey

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Film Reference J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimal 1497 1378 AATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCA 1437 312 300 360 GAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCCAGAGTGGATGGTCCAACAC 132 432 Gaps 9 72 GAGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAAACT 1438 GAACTTCTCCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGAT 133 ACACTCCACGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAGACAAGTGTGGCA 181 ACAGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATC TGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCTTCCGGCGGCAAA rerereadeceartracacadadecerrecadacreadaceadacereregrada 361 radacarrrriccracarcescrrecereracacereaacacacrerarrrearressece CATAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACTTCACC GAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGAT 13 CGGCCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGCGCCCTGCCTCGA ccesceanerecercerecraecerecerecerererecadadececeracea 121 GATCTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCA GCAGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCAGACGCCAGCATC 15; 49.1%; Score 963.6; DB 9; Length 78.7%; Pred. No. 3e-313; ive 0; Mismatches 309; Indels

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430RIDS: US/10/175,737
CURRENT APPLICATION WUMBER: 2002-06-19
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Pred. No. 3e-313;
0; Mismatches 309;
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US-10-175-737-399; Sequence 399, Application US/10175737; Publication No. US20030013153A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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ilarity 78.7%;
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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US-10-175-737-399
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Matches 1194; Conserv
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US-10-063-502-157
Sequence 157, Application US/10063502
Publication No. US20030023042A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
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APPLICANT: Goodwaki, Paul J.
APPLICANT: Goodwaki, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Granabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE PREPRINCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NOS: 170
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Pred. No. 3e-313;
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Matches 1194; Conservative
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; ORGANISM: Homo Sapien
US-10-063-502-157
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| Publication No. US20030022293A1
| Publication No. US20030022293A1
| GENERAL INFORMATION:
| APPLICANT: Baker, Kevin P. |
| APPLICANT: Desnoyers, Luc |
| APPLICANT: Godowski, Paul J. |
| APPLICANT: Godowski, Paul J. |
| APPLICANT: Pan, James |
| APPLICANT: Watanabe, Colin K. |
| APPLICANT: Zhang, Zemin |
| APPLICANT: Zhang, Zemin |
| ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Pred. No. 3e-313;
0; Mismatches 309;
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TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper (NUMBER OF SEQ ID NOS: 612
LENGTH: 1515
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.7%;
Matches 1194; Conservative (
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US-10-173-706-399
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Search completed: May 28, 2003, 10:37:20 Job time : 233.213 secs

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MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
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STRANDEDNESS: single
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Compugen Ltd.
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US-09-346-408-5

US-09-232-465-14

US-09-261-416-1

US-09-261-416-1

US-09-218-046-3

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                 GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 258; Indels
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
SUSPENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
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0.008;
                                                                                                                                                                                                                                                                                                                   Score 44.2;
Pred. No. 0.
                                                                            STRAIN: IL-17 R (hCTLA8 receptor)
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                                                                                                                                                                                                                                                                                                                   Query Match 2.3%;
Best Local Similarity 45.1%;
Matches 224; Conservative
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MEDIUM TYPE: Floppy disk
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ORGANISM: Hur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 258; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3223;
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Pred. No. 0.008;
                                                    FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                               USSN 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REPERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GITGAAGTGAATTTCAC 614
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.39
Best Local Similarity 45.19
Matches 224; Conservative
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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93..2693
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ORIGINAL SOURCE:
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, LOCATION:
US-09-022-255-9
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298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGA 357
                                                                                                                                           358 CCTTCCGGCGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTC 417
                                                                                                                                                                                       501 CATCACCACAGGCGGTGGCGTTTTACCTTCAGCCACTTTGTGGTTGACCCTGACCAGGAA 560
                                                                                                                                                                                                                                                                                      561 TATGAGGTGACCGTTCACCACCTGCCCAAGCCCATCCCTGATGGGGACCCAACCACCAG 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                    538 ACTGAGGCGGGAAGCCTGTGGGACCCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATG
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APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                           441 criccacrigaacaarigaacerrrerecercaegerrreagrirrererecaaacreage
                                                                                                                                                                                                                                         478 TCTGTGAACTTCACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGC
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396 ACAGACGCCAGCATCCTGTACCTCGAGGGTGCAGAGTTATCTGT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacinitosh
OPERATING SYSTEM: Apple Operati
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-978-773-3; Sequence 3, Application US/08978773; Patent No. 6083906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/0:
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 GTTGAAGTGAATTTCAC 614
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ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 AAGACAAGTGTGGCAGCAGAGGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGG 237
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                                                                                                                                                                                                         No. 6072037el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKINER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                 STATE: WA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                   Sequence 9, Application US/09022696
Patent No. 6072037
                                                                                                                                      APPLICANT: Yao, Zhengbin
APPLICANT: Sprisgs, Melanie
APPLICANT: Fanelow, William
TITLE OF INVENTION: No. 60720:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporat:
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(206)
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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ZIP: 98101
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; LOCATION:
US-09-022-696-9
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                                                 US-09-022-696-9
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598 GTTGAAGTGAATTTCAC 614
                                                                 PRIOR APPLICATION
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ORIGINAL SOURCE:
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HYPOTHETICAL:
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TELEFAX: (
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; LOCATION:
US-09-022-253-9
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Best Local
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                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                      Length 3223;
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Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                    0; Mismatches 258; Indels
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      Score 44.2; DB 3;
Pred. No. 0.008;
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51 University Street
                                                                                                                                                                                                                                                  2.3%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                      Best Local Similarity 45.1
Matches 224; Conservative
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                                                                                                                                                             93..2690
ORGANISM: Human
                             IMMEDIATE SOURCE:
CLONE: IL-17R
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                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-978-773-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-022-253-9
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STATE:
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                                                                                               FEATURE
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178 AAGACAAGTGTGGCAGCAGCAGTTTTTCAATTTTGATGAACATAAGCTGGATACTCCGG 237
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Pred. No. 0.008;
0; Mismatches 258; Indels
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USSN 08/410,535
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STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                       FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/PILING DATE: 23 MARCH 1995
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 587-0430
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TYPE: nucleic acid
STRANDEDNESS: single
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93..2693
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298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGA 357
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                            238 GCAGACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAAC 297
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Sequence 9, Application US/09022259

Patent No. 6191104

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE.OF INFORTION: No. 6191104el Receptor That Binds IL-17

NUMBER OF SEQUENCE: 10

CORRESPONDENCE ADDRESS:
                                                                       396 acadaceccadearcereracerceaderecadarrarerer----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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APPLICATION NUMBER: 08/620,694
FILING DATE:
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AAGACAAGTGTGGCAGCAGCAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGG 237
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45.1%; Pred. No. 0.008;
iive 0; Mismatches 258; Indels 15
                                                                                                                                                                                                     APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Miliam
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 981u.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
..... Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft word for Apploure
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filling Description:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-
TELECOMMINICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                               E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
                                                                                                                                     Sequence 9, Application US/09022260 Patent No. 6100235
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741 CTGCGTGTGAGCTTCAC 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                  GENERAL INFORMATION:
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STREET: STATES TO STATES TO STATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
US-09-022-260-9
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Sea
STATE: WA
COUNTRY:
                                                                                                                  US-09-022-260-9
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COMPUTER READABLE FORM:
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, LOCATION:
US-09-022-257-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
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Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yea, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44.2; DB 4; Length 3 Pred. No. 0.008; 0; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 ACAGACGCCAGCATCCTGTACCTCGAGGGTGCAGAGTTATCTGT---
                                                                                                                                                                                                                                                                               ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
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STREET: 51 University Street
CITY: Seattle
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.1%;
Matches 224; Conservative
3223 base pairs
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                             TYPE: nucleic acid
STRANDEDNESS: single
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93..2693
                                                                                                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seatt
STATE: WA
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-09-022-259-9
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TGGATGGTCCAACACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 TTTGCCCACACCCAACAAGGAGACCTGTTCCCCGTGGCTCACATCGAATGGACACTGCAG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 GCAGACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGA 357
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Pred. No. 0.008;
0; Mismatches 258; Indels 15
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 ACAGACGCCAGCATCCTGTACCTCGAGGGTGCAGAGTTATCTGT
                                                                                                                                                                                                                                                                                                                                                         USSN 08/410,535
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STRAIN: IL-17 R (hCTLA8 receptor)
                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIPECATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: USSN 08/41(
FILING DATE: 23 MARCH 1995
CLASSIPICATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 3223 base pairs
nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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93..2693
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Best Local Similarity
Matches 224; Conserv
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
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RESULT 11
US-08-232-463-14/c
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                                                                                                                                                                                  US-08-872-302-3
; Sequence 3, Application US/08872302
; Patent No. 5846784
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. duPont de Nemours and Co.
; STREET: 1007 Market Street
; STREET: 1007 Market Street
; STATE: Delaware
; COUMTRY: USA
                                   681 ATGAGCTCAGGCAGCCTGTGGGACCCCAACATCACGTGGAGACCCTGGAGGCCCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.9%; Score 38; DB 2; Length 1364; Best Local Similarity 71.4%; Pred. No. 0.33; Matches 50; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BE-1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-346-408-5
Sequence 5, Application US/09346408B
Patent No. 6338966
GENERAL INFORMATION:
APPLICANT: Allen, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                   741 CIGCGTGTGAGCTTCAC 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1364 base pairs
                                                                       598 GITGAAGIGAATTTCAC 614
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STRANDEDNESS: single
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 AAAAAAAAA 1357
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; LOCATION:
US-08-872-302-3
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1877 ATGCTGCACGTAGACCGTTTTGTAACATTTTAATCTGTTAATGAATAATCCGTTTGGGAA 1936
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APPLICANT: Rafalski, Antoni
TITLE OF INVENTIVO: Genes Encoding Sulfate Assimilation Proteins
FITLE OF INVENTIVO: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
CURRENT APPLICATION NUMBER: US/09/346,408B
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION WUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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Pred. No. 0.56;
0; Mismatches 31; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1937 GCTCTCAAAAAAAAAAAAAAAAAAAA 1963
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
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TELEPHONE: (703)836-9300
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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Best Local Similarity 64.4%;
Matches 56; Conservative
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Glycine max
US-09-346-408-5
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STRANDEDNESS:
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NAME/KEY: CDS
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                                     US-09-261-416-1
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US-09-518-046-3
                                                                                                                                                                                                                                                              SEQ ID NO 1
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                                                                                                                                              511 CACGTAATGAAATATAAAAAGCAGTGCACTGAGGCGGGAAGCCTGTGGGACCCCAGACATC 570
                                                                                                                                                                                                                     571 ACTGCTTGTAAAAGAACGAGAAGATGGTTGAAGTGAATTTCACAACCAATCCCCTTGGA 630
                                                                                                                                                                                                                                                                                                                                                                 691 AATAAACTGATGAGGACGTCTGTAGCCATCCCGGTGACTGAGGAGAGTGAAGGTGCGGTG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITGIGCITIGCTCAGAGACAAGTGCTCCCATCCCTCCAGATGACAACAGACGCATGCTG 870
                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         751 GTTCAGCTGACCCCATATTTACATACCTGCGGCAATGACTGCGTCCGACGCGAAGGGACA
                                                                          1.9%; Score 37.4; DB 1; Length 7218; 3.6%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%; Score 37.2; DB 4; Length 2413; 63.3%; Pred. No. 0.77; Live 0; Mismatches 33; Indels 0.
                                                                                                              Indels
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NAME/KEY: CDS

OTHER INFORMATION: entire CDNA sequence of TADG-12 gene
US-09-218-046-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1. Application US/09518046

Patent No. 629463

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Transmembrane Serine Protease Ove:
TITLE OF INVENTION: Transmembrane Serine Protease Ove:
TITLE OF INVENTION: In Ovarian Carcinoma and Uses The;
CURRENT APPLICATION NUMBER: US/09/518,046

CURRENT APPLICATION NUMBER: 09/261,416

EARLIER PILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 153
                                                                     Query Match
Best Local Similarity 3.6%; Pred. No. 1.2;
Matches 14; Conservative 209; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1075 RRRRRRRRRATCGCAGCTCCACCTGCAG 1043
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Matches 57; Conservative
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ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2413
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Sequence 1, Application US/09261416A

Patent No. 6291663

GENERAL INFORMATION:
APPLICANT: 0'Exiten, Timothy J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILER REPERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1874 TCTATGCTGCACGTAGACCGTTTTGTAACATTTTAATCTGTTAATGAATAATCGGTTTGG 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2316 TCTTTGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCCAAATAATATGTTCC 2375
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| Patent No. 6294663
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| APPLICANT: Underwood, Lowell J.
| TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
| TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
| FILE REFRENCE: D6192CIP
| CURRENT APPLICATION NUMBER: US/09/518,046
| CURRENT PILING DATE: 2000-03-02
| EARLIER APPLICATION NUMBER: 09/261,416
| FARLIER FILING DATE: 1999-03-03
| SEQ ID NO 3
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US-09-518-046-3
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Best Local Similarity 63.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 NCKNACRICRIGNARNCCNARRTANACNGTNACRIGYTCYTINSWNACNGGDAINACNGT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 NGTRITCNCKNCKYTGNSWNCKNARNACRTGNGCNGTNARDATCCANSWNGCNSWNAR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence CARANISM: Artificial Sequence CARANISM: Artificial Sequence CARANISM: PEATURE: PEATURE: OTHER INFORMATION: Sequence of SEQ ID NO:2.
NAME/KEY: variation
LOCATION: (1)...(807)
COTHER INFORMATION: N is any nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 36.2; DB 4; Length 807;
Best Local Similarity 27.9%; Pred. No. 0.86;
Matches 81; Conservative 37; Mismatches 172; Indels 0
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Patent No. 6423526
GENERAL INFORMATION:
APPLICANT: HOLloway, James L.
TITLE OF INVENTION: Human Serine Protease
FILE REFERENCE: 99-88
CURRENT APPLICATION NUMBER: US/09/715,994
CURRENT FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 28, 2003, 10:22:39
Job time : 118.256 secs
RESULT 15
US-09-715-994-3/c
                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 807
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     1963
1472.2
989.8
988.2
988.2
988.2
982.4
980.8
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seq
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length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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Human IL-17R cDNA.	Human IL-17R cDNA.	OD.	Human interleukin-	Mouse spliced tran	Human interleukin	HETCC45RA cDNA clo	cDNA clone sequenc	Human interleukin	HHPCH63R cDNA clon	clone	Mouse DCRS6 revers	Human ovarian canc	Human colon cancer	Human colon cancer	Human IL-17RH cDNA	Human reproductive	Human cytoskeletal	_	Human immune syste	•	•	Mouse DNAX cytokin	Human IL-17 recept	cDNA encoding huma	Human secreted pro			Human DCRS6 revers	Human interleukin	cDNA encoding inte	cDNA encoding a hu	Human PRO5801 cDNA		Human DNA encoding	cDNA encoding inte

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## ALIGNMENTS

Mouse interleukin-17 receptor related protein (Evi27) encoding cDNA #1

06-NOV-2001 AAD13445;

(first entry)

RESULT 1 AAD13445

AAD13445 standard; cDNA; 1963

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02-FEB-2001; 2001WO-US03518.
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P-PSDB; AAE07162.
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The present sequence is a cDNA encoding mouse interleukin (II): receptor related protein (Evi27). Mouse Evi27 gene was mapped to chromosome 14. Evi27 is a common site of retroviral integration in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are uses
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/transl_except= "(pos:162..163, aa:Cys-Leu)"
/note= "Insertion of 626 bases alters the res
frame; CDS does not include stop codon"
/partial
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Matches 1474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as antisense molecules to inhibit Evi27 protein or for chromosomal mapping or mutational analysis of Evi27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as II-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of Evi27 at the RNA or protein level is used in the treatment of diseases such as cancer or autoimmune diseases.
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/product= "CDS is specifically is claimed in claim 3"
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                                                                                                                                                                                                                                                                                                                                       The present sequence is human protein with hydrophobic domain encoding CC cDNA clone HP10758. The polynucleotide and polypeptide of the invention CC may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The CC polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The CC polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and CC supplements, to modulate orytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of CC microbial infections and autoimmune disorders such as multiple sclerosis, remanatoid arthritis and insulin-dependent diabetes), to modulate change it is disease and Alzheimer's CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's CC disease), to modulate activin and inhibin activity, to modulate receptor cCC modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
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12-MAY-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. cozema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischammia), eye disorders, reproductive disorders, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; II-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Three human nucleic acids encoding interleukin 17 (IL-17) receptor polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections) -
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           The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the
                                                                                                                                                                                                                                                                                                                                                                                                              Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in respective of increased protein levels or immunological disord
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                                                                                                                                                                                                                                                                                                                                                             biodiversity;
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; 2000US-0631451.
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Best Local Similarity 77.9%;
Matches 1241; Conservative
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P-PSDB;
                                                                                                            The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
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                                                                          Sequence
                                                                                                                                                                                                                                     Isolated polypeptide for treatment antibodies and research use -
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8 S S 밁 밁 밁 밁 S 밁 S 밁 S 밁 Ś 밁 á 片 S 밁 Ś 밁 544 484 364 604 615 555 495 424 435 375 304 315 244 255 184 195 124 135 64 75 4 AACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACATTGGGGTT GTGGGACCCAGACATCACTGCTTGTAAAAAAGAACGAGAAGATGGTTGAAGTGAATTTCAC GCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAAGCAGTGCACTGAGGCGGGAAGCCT TAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTC TAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGTGAACTTCACCTC GACATTTTCCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCCA GACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCCCA TGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCTTCCGGCGGCAAATG CTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATGAATTCATACAGCTG TCTAATCCCGGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTTGCAAC GCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGA ACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAAGTGTGTCAAGGCCGGAAGCCT TGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCCAGACCCTCTGGTGGTAAATG CTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTG AGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCG AGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCAGACGCCAGCATCCG ACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAGACAAGTGTGGCAGC GCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGTCCAACACAC GGCGATGTCGCTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGA 674 554 183 134 603 614 543 483 494 423 434 303 314 243 254 194 63 363 374

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The present sequence is a cDNA encoding human interleukin (II)-17 (CC receptor related protein (Bvi27). Human Evi27 genee was mapped to chromosome 3p21. Evi27 is a common site of retroviral integration CC in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful as antisense molecules to inhibit Evi27 protein or for chromosomal companion or mutational analysis of Evi27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of Evi27 at the RNA or protein level is used in the treatment of diseases such as cancer cor autoimmune diseases.
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The present sequence encodes a human interleukin 17-receptor-like pr (ILITRLP) variant. The ILITRLP polypeptide is useful for screening f agonists and antagonists. These antagonists and agonists are useful treating, diagnosing, detecting and or preventing disorders related cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythromatosu

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                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                 product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA; 1918
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                                                                                                                                                                                 "Interleukin-17
                                                                                                                                                                                                                                                                                                                                                                                                                           hematopoietic; proliferative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent relates to novel interleukin-17-like receptor

C protein (II-17RLP). II-17RLP is a homologue of the II-17 receptor and has

C a wide range of cytokine receptor-like activities. II-17RLP or its

C asyonists may be used to enhance host defenses against resistant chronic

C and activation of microbicidal leukocytes. I may also be used to

C increase T-cell proliferation by stimulating II-2 biosynthesis, for the

C treatment of T-cell mediated autoimmune diseases and lymphocytic

C leukaemias. II-17RLP may also be used to regulate hematopoiesis and to

C treat sepsis. Extracellular II-17RLP domains may be used as antagonists

C of II-17RLP. II-17RLP agonists and antagonists can also be used to

C modulate II-6 expression, useful in treatment of cancers such as

C myelomas, plasmacytomas and hymridomas and Lennert's Lymphoma. The

C myelomas, plasmacytomas and hymridomas and Lennert's Lymphoma. The

C myelomas, plasmacytomas and hymridomas and Lennert's Lymphoma. The

C myelomas squence encodes human II-17RLP. This cDNA sequence was

C derived from sequencing the HAPOR40 cDNA clone (ATCC deposit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sig
Matches 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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16-SEP-1998;
16-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 141-143; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides encoding interleukin-17-like receptor protein, useful for diagnosis and treatment of immune system-related disorders, e.g. sepsis and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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DB; AAY70595.
                                                                                                                      TGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
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                      CATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACC
                                            CATAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGTAACTTCACC
                                                                                                                                                                                                                TGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCTTCCGGCGGCAAA 372
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98WO-US19121.
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1 AGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGG	/ 150	Ş
AGCAGGAAAAAGATCACAAGCCTGCCA	154	멍
1 GAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGAT 1500	144	ð.
CTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTG	0 148	<u>.</u>
1 AATGCCCTGAGTGTCTGCCCCCAATATCATCTCATGAAGGACGCCACAGCTTTCCACACA 1440	/ 138	,Q
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ATCTGCACAAATACCTGGTG	/ 132	Ş
CTCTCAAGA-CTCTTCCCCCTTGCCTTTTAACCTTTTCTGCAGTGATCTAAGAAGCC	136	문
AGGÀTCTGTTCCCTTTGCCTTTAACCTCTTTTGTAGTGATTTCAGCAG	/ 126	Ş
ATGACGTCAACAGTGTGTGCGATGGTACCTGTGGC		밁
AGTGACGTCCCGACCCTTTGTGACAGTGCCTGTGGCCACAATGAGGGCAGGCCAGGG	/ 120	Ş
2 CCAGTGCAGTGGCTTGCCACTCAAAAGGAAGGCAGACAAAGTCGTCTTCCTTTCC 1301	124	da
CGGTACAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGGTCTTCCTTC	/ 114	S S
rccttgaaaagtggcagaaaaagaaaatagcagag	118	뭣
TGCAGAAGTGAGGTCATCCTTGAAAAATGGCAGAAAAAGAAAATCGCCGAGATGG	/ 108	Ş
2 TACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAAAC 1181	0 112	밁
TCCTTCTGAGATATGTTTCCATCACACCGTCTGTCGCTTCACTGACTTTCTTC	/ 102	,Q
5 AAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCCATTAAGGTTCTTGTGGTT 1121	106	망
ACGICCTITCCIATITCCACCATGCICCTGCCCCTCATIAAGGICCTGGTGC	/ 96	,Q
05 CTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATC 1064	10	ర్జ
1 CTGGTGGCTGTGTGGGTGGCAGCTGGGAACTTACCTTAC	90	ĮQ.
5 CCTCTGGATAACAAAAAGCAAGCCGGGAGGCTGGCTGCCTCCTCCTGCTGTCTCTG 1004	94	贯
CTCCAGATGACAACAGACGCATGCTGGGAGGCTGGCTGCCTCTCTTCCTGGTG	84	Q
S AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCG	88	망
CTGCATCCGACGCGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGCTCC	78	,Q
5 GTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGCATATTTTCCTACTTGTGGC 884	82	ďq
TGACTGAGGAGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTACATACCTGCGG	72	δ O
ACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTC	76	Дb
AGAATAAACTGATGAGGACGTCTGTAGCC	/ 67	Ş
5 ACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGG 764	70	Db Db
ACAACCAATCCCCTTGGAAACAGATACACGGTTCTCATTCAACGGGACAC	/ 613	S S
S CTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTC 704	64	뮍
TGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAGAGA	, 55	δõ
5 TCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAA	58	뮍
AGTGCACTGAGGCGGGAAGC 5	49	δ

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25-APR-2000; 2000US-199550P

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25-APR-2000; 2000US-199550P

25-APR-2000; 2000US-199544P

03-MAY-2000; 2000WO-US13705

22-MAY-2000; 2000WO-US14941

02-UUN-2000; 2000WO-US15264

05-UUN-2000; 2000US-209832P

28-AUG-2000; 2000US-0544848

24-AUG-2000; 2000WO-US23328

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                                         ) GENENTECH INC.
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2000US-196690P.
2000US-196820P.
2000US-198121P.
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2000US-199550P.
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2000US-194449P.
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Baker KP, cuc.

Chen J, nith V, V

Watanabe

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Godowski PJ,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the chivention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of comparing the level of expression in the test sample indicates the presence of a chigher level of expression in the test sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a cumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human could be protected with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, colon, proteins, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1194;
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Best Local (
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                                                                            TCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACTGAGGCGGGAAGC
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                                    CTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTTGAAGTGAATTTC
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02-JUN-2000;
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GENENTECH INC

Chen .,
Gurney AL, Li Filvaroff E, ru.,
Li H, Hillan KJ, Fong S, Goddard A, Godowski l lan KJ, Tumas D, Van Lookeren PM, Wood WI, Yansura DG; η M, Grimaldi Vaņdlen F CJ;

P-PSDB; 2001-451708/48. DB; AAU04955.

Novel PRO polypeptides homologous diagnosis and treatment of immune arthritis and diabetes to interleukin-17, useful for the related disease e.g. rheumatoid

Claim 1; Fig 11; 188pp; English

systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated rena disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification. The sequence (DNA 115291-2681) encodes a PRO polypeptide (PRO5801) which is the human Interleukin 17 receptor, IL-17KH1. A composition containing ant/agoniets to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. renal S, an

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                                                                                                          CATAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACTTCACC
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                            ACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACATTGGGG
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ACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGG
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Pred. No. 6.8e-285;
0; Mismatches 309;
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Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis; cellular activation; haemostasis; angiogenesis; tumour metastasis;

cDNA encoding a human interleukin 17 receptor-like polypeptide

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                                                                                       GAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGAT
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                                                                                                                                                                                                                                                                                                                                                                                              family, an treating,
                                                                                                                                                                                                                                                                                       cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythromatosu
                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP polypeptide is useful for screening f agonists and antagonists. These antagonists and agonists are useful treating, diagnosing, detecting and or preventing disorders related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
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                                                  CGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATGAATTCATACAGC
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                                                                                                                                                      GAGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACAT
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Pred. No. 7.6e-285;
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Novel polynucleotides encoding interleukin-17-like receptor useful for diagnosis and treatment of immune system-related
                                  P-PSDB; AAY70591.
                                            WPI; 2000-271403/23
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                                                                                        GENOME
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                                                                                                             98US-0154219.
98WO-US19121.
99US-0268311.
                                                                                                                                                          99WO-US21048
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                                                                                                                                                                                                                                                                                                                                           /*tag= /
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                                                                                                                                                                                                                                                                          /product= "Mature IL17RLP" 52..1287
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/note= "This is an alternative mature protein"
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The patent relates to novel interleukin-17-like receptor CC protein (IL-17RLP). IL-17RLP is a homologue of the II-17 receptor and has a wide range of cytokine receptor-like activities. II-17RLP or its caponists may be used to enhance host defenses against resistant chronic and activation of microbicidal leukocytes. It may also be used to and activation of microbicidal leukocytes. It may also be used to cincrease T-cell proliferation by stimulating IL-2 biosynthesis, for the creatment of T-cell mediated autoimmune diseases and lymphocytic concentrates. II-17RLP may also be used to regulate hematopoiesis and to creat segsis. Extracellular II-17RLP domains may be used as antagonists of II-17RLP. II-17RLP agonists and antagonists can also be used to condulate II-6 expression, useful in treatment of cancers such as composition of concers such as concerns of the concerns of concerns of the concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of concerns of c
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                                                             ACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGG
                                                                                ACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACACTGGGG
                                                                                                                           CTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAACTTC
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TTTTCTCAGGTGTTTGAGCCACACCÁGAAGAAÁCAAACGCGAGCTTCAGTGGTGATTCCA
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Search completed: May 28, 2003, 00:09:24 Job time : 412.851 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database : Post-processing: Minimum Match 0%
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Listing first 45 summaries Minimum DB Maximum DB Run on: OM nucleic - nucleic search, using sw model Total number of hits satisfying chosen parameters: Searched: Scoring table: Title: Perfect score: seq length: 0 seq length: 2000000000 May 27, 2003, 22:37:09 ; Search time 4999.22 Seconds (without alignments)
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## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 AF208108
<pre>1 (bases 1 to 1963) Tian,E., Sawyer,J.R., Largaespada,D.A., Jenkins,N.A., Copeland,N.G. and Shaughnessy,J.D. Jr.</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus.		AF208108.1 GI:9246428	AF208108	complete cds.	Mus musculus IL-17 receptor homolog precursor (Evi27) mRNA,	AF208108 1963 bp mRNA linear ROD 17-JUL-2000	

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Direct Submission
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/note="putative"
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LRDLQVELVKTSVAAEBFSILMNISWILAADASIRLLKATKICVGGKUNNNSYSCVRC
NYTEAFQSQTRPSGKWTFSSYGFPPELSTLYLISAHHIPHANNNEDSPSESLSVHETSE
GCLNHWKYKKQCTEAGSLWDPDITACKKNEKNVEVNFTINPLGNRYTILIQRDTTLG
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PDNNRRMLGGMLPLFLYLVANWYLAAGIYLTWRQGHSTKTSFPISTMLLFLIKVLVY
YPSEICFHHTVCRFTDFLQNYCRSEVILEKWQKKKIAEMGPVQWLTTQKQAADKVVFL
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492 c
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/note="putative GSK3; phosphorylation
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KGDYNALSVCPQYHLMKDATAFHTELLKATQSMSVKKRSQACHDSCSPL"
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/protein_id="AAF86049.1"
/db_xref="GI:9246429"
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/db_xref="taxon:10090"
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 GCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATGAATTCATACAGCT
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Query Match
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Sequencing Group at the Stanford Human

Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
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Direct Submission

Direct Submission

Submitted (02-APR-2002) National Institutes of Health, Mammalian Submitted (02-APR-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution informat
through the I.M.A.G.B. Consortium/LINI at: http://i
Series: IRAK Plate: 58 Row: m Column; 5
This clone was selected for full length sequencing
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LPSDVPTLCDSACGHNEGSARENSQDLFPLAFNLFCSDFSQTHLHKYLVVYLGGADL
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35 a 504 c 501 g 478 t
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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db_xref="taxon:10090"
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Shaughnessy, J.D. Jr.
Direct Submission
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Mammalia; Eutheria; Roc
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Tian,E., Sawyer,J.R., I
and Shaughnessy,J.D. Jr
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217. .219
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/note="putative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTTTGGGAAGCTCTCAAAAAAAAAAAAAAAAAAAAA 2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Grereira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Grands, B., Goyette, M., Graham, L., Grand-Pierre, N., Grands, G., Goyette, M., Graham, L., Grand-Pierre, N., Grands, G., Goyette, M., Graham, L., Grands, P., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., Grands, G., G
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Mus musculus, clone RP23-25A7
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1 (bases 1 to 234131)
Birren,B., Linton,L.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 234131)
                                                                                                                                                                                                                                  Insert size: 210000; agarose-fp
Insert size: 232831; sum-of-contigs
Quality coverage: 10.4 in Q20 bases; agarose-fp
Quality coverage: 9.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.960731
Consensus quality: 225885 bases at least Q40
Consensus quality: 23172 bases at least Q30
Consensus quality: 231921 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L13729
Center clone name: 25_A_7
Center clone name: StatIstics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 10 Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
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, WORKING DRAFT SEQUENCE, 14 unordered
         contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n/a; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research
                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                            BASE COUNT
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Query Match
Best Local Similarity
Matches 1000; Conserv
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vector_side:1
                                                   50.5%;
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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105250 106522: contig of 1273 bp
106523 106622: gap of 100 bp
106623 108946: contig of 2324 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137591 137690: gap of 100 bp
137691 150406: contig of 12716 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129390 129489: gap of 100 bp 1129490 137590: contig of 8101 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108947 109046: gap of 100 bp
109047 110758: contig of 1712 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233880 233979: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150407 150506: gap of 100 bp
150507 233879: contig of 83373 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121327 121426: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113411 113510: gap of 100 bp 113511 121326: contig of 7816 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l10759 110858: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 847 2105: contig of 1259 bp in length
2106 2205: gap of 100 bp
2206 3019: contig of 814 bp in length
3020 3119: gap of 100 bp
3120 105149: contig of 102030 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            747 846: gap of
847 · 2105: cc
                                                                                                                                                                                    /note="assembly_fragment"
233980. .234131
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
110859. .113410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
106623. .108946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                             note="assembly_fragment"
50507. .233879
                                                                                                                                                                                                                                                                         note="assembly_fragment'
.37691. .150406
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129389: contig of 7963 bp
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113410: contig of 2552 bp in length
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Score 991.6; DB 2;
Pred. No. 3.9e-288;
0; Mismatches 14;
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DEFINITION
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Best Local Similarity
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CTTCACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAAGCAGTGCACTGAGGC
                                                                                                 CAGCGCCCATAACATCCCCCAATGCTAATATGAATGAAGGACAGCCCTTCTTTGTCTGTGAA 485
                                                                                                                                                                                         CGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCAT
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                                                                       TGGGGCCCATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAA
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Patent: WO 0149728-A 56 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL
Location/Qualifiers
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1 (bases 1 to 1818)
Kato,S. and Kimura,T
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//protein_id="CAC51160.1"
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//db_xref="od:15209722"
//db_xref="od:15209722"
//db_xref="od:15209722"
//translation="MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLLYGPVELNITVYFIGAHNIPNANMEDGPSMSVNFTSP
GCLDHIMKYKKKCVKAASSLWDPNITACKKNEETVEVNFTTTPLARKMYMALIQHSTIIG
FSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGV
PFPLDNNKSKPGGWLFLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLPPIKV
PFPLDNNKSKPGGWLFLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLPPIKV
VVFLSBUNNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFRE
IDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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Pred. No. 7.5e-288;
D; Mismatches 337;
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Patent: WO 0168705-A 1 20-SEP-2001;
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                                                                                                                        CGACTATAATGCCCTGAGTGTCTGCCCCCAATATCATCTCATGAAGGACGCCCACAGCTTT
                                                                                                                                                                                 CAGCCAGACGCATCTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGGTTTACCCATCTGAAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCT
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CCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAA--TAGAGACTCTGAAGCCTTC
                                                                                                                                                               AAGCCAGATTCATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTGATACAAAAGA 1413
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                                                                                                                                                                                                                                                                                                                                             GATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCT
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                                                                                                       CGATTACAATGCTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
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                                                                                                                                                                                                                                                                                                                                                                 CAGTGGCCGGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGCGCCCT
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Il-17 molecules and uses thereof
patent: WO 0208285-A 17 31-JAN-2002;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PFPLDNNKSKPGGWLFLLLSLLVATWVLVAGIYLMWREREIKKTSFSTTTLLPPIKV
PFPLDNNKSKPGGWLFLLSLLVATWVLVAGIYLMWREREIKKTSFSTTTTLPPIKV
VVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKKVVVVFRE
IDTKDDYNALSVCPKKHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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/db_xref="taxon:9606"
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Pred. No. 2.3e-287;
D; Mismatches 338;
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Catarrhini; Hominidae;
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                                  CGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
                                                                                                     CAGTGAGAACTCTCAAGACCTCTTCCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: n Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9246432.

1. .2042
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Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-NOV-2000) National Institutes of Health, Mammalian Submitted (16-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2042)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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GCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTIIG
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                                                                                                                                                                                                                                                                                                                                        'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                       note="Vector:
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	958 AGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTGGTG 1017	8
	898 CTGCTGGTGGCTGTGTGGGTGCTGGCAGCTGGGATCTACCTTACCTTGGAGGCAAGGAAGG	유 성
	841 ATCCCTCCAGATGACAACAGACGCATGCTGGGAGGCTGGCT	유 성
	781 GGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGCTCCC 840	유왕
	721 CCGGTGACTGAGGAGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTACATACCTGC 780	B 6
	670 GGGTTTTCTAGAGTGCTGGAGAATAAACTGATGAGGACGTCTGTAGCCATC 720	당 성
	610 TTCACAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACATTG 669	음 성
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	490 ACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACTGAGGCGGGA 549 	유 성
	430 GCCCATAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACTTC 489	B 8
	370 AAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGC 429	B &
	310 AGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCTTCCGGCGGC 369	유정
	250 ATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATGAATTCATAC 309	B 8
	190 GCAGCAGAGGAGTITTCAATITTGATGAACATAAGCTGGATACTCCGGGCAGACGCCAGC 249	유 성
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	70 CGAGAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGTCCAA 129	음 성
	10 GGCCGGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGCGCCCTGCCT 69	유정
4	Query Match 50.2%; Score 985.8; DB 9; Length 2042; Best Local Similarity 77.9%; Pred. No. 1.2e-286; Matches 1245; Conservative 0; Mismatches 337; Indels 17; Gaps	Z W Q
	E COUNT 625 a 484 c 426 g 507 t	BASE ORIG

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	RESULT 9 AX350967 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES BOURCE		8 8 8 8 8	8 8 8 8 8	04 04 04 05
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Query Match  Query Match  Best Local Similarity 77.8%; Pred. No. 4e-285;  Best Local Similarity 77.8%; Pred. No. 4e-285;  Matches 1240; Conservative 0; Mismatches 37; Indels 17; Gaps 4;  Qy 15 GGCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGAGAGCGCCTGCCT	polyA_signal 1643.1649 /gene="EVI27" polyA_signal 1781.1786 /gene="EVI27" polyA_site 1796 PolyA_site 1796 BASE COUNT 548 a 438 c 397 g 445 t		sig_peptide 64  /gene="EVI27"  mat_peptide 451511 /gene="BVI27"  /gene="BVI27" /product="IL-17 receptor homolog"  misc_feature 204206 /gene="BVI27" /note="putative; glycosylation site" /gene="BVI27" /note="putative; glycosylation site" /gene="BVI27" /note="putative; glycosylation site"		/Chromosome="3" /map="3p21" gene 11828 /gene="EVI27" /note="linked to ecotropic viral integration site 27 in myeloid leukemias" CDS 61514	Center, University of Arkansas for Medical Sciences, 4301 W.  Markham St, Little Rock, AR 72212, USA FEATURES Location/Qualifiers Source 1. 1828  /organism="Homo sapiens" /db_xref="taxon:9606"
Qy 1023 TCCTTCTGAGATATGTTTCCATCACACCGTCTGTCGTTCACTGACTTACTAAACTA	903 903 963	Db 662 TTCTCAGGTGTTTGAGCCACACCAGAAGAACGCGGAGCTTCAGTTGTGGTGATTCCAGT  Qy 726 GACTGAGGAGATGAAGGTGCGGTGGTTCAGCTGCGCCATATTTACATACCTGCGGCAA	Db 482 ACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAAA	315 302 375 362 435 422 495	Oy 195 AGAGGASTITICAATITIGATICAAGCTIGATIACTICGGGCAGAATICGGCCAGCATICGGCCAGCATICGGCCAGCATICGGCCAGCATICGGCCAGCATICGGCCAGCATICGGCAGCATICGGCCAGCATICGGCCAGCAGATICGAGCTAGAGTTTGAATTTTGATGAATGTAAGCTGGGGCAAAAACAACATGAAGTTCCAGCTGGCGCAGACATGAAATTCAATACAGCTGGCGCAAAAAACAACATGAAATTCAATACAGCTGGCGCAAAAAACAACATGAAATTCAATACAGCTGGCGCAAAAAACAACATGAAATTCAATACAGCTGGCGCAAAAAACAACATGAAATTCAATACAGCTGCAGCTGGCCTGCAAAAGGCAACTTCCAGTCCTACAGCTGCAAAATTCAAAAGGCAACTTCCAAGTTCTACAGCTGCAAAAAGCAACTTCCAGTCCTACAGCTGCAAAAGGCAACTTCCAAGTTCTACAGCTGCAAAAAGCAACTTCCAAGTTCTACAGCTGCTGAAAAGGCAAAAAAGCAACTTCCAAGTTCTACAGCTGCTAAAAGGCAAAAAAGCAACTTCCAAGTTCTACAGCTGCTAAAAAGCAACTTCCAAGTTCTACAGCTGCTAAAAAGGCAACTTCCAAGTTCTACAGCTTGCAAGTTTGTGTGTG	135 122

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Query Match Best Local Similarity 78.7%; Pred. No. 6.3e-280; Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;  Qy 13 CGGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCAGCAGCAGCCCTGCCTCGA 72	DEFINITION Sequence 399 from Patent WO0168848.  ACCESSION AX376332 VERSION AX376332.1 GI:19170557 KEYWORDS SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 RITILE Baker, K. P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P. J., Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Patent: WO 0168848-A 399 20-SEP-2001; FEATURES SOURCE /organism="Homo sapiens" / Ob_xref="taxon:9606" BASE COUNT 404 a 384 c 363 g 364 t	QY 1141 CCGGTACAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGGTCTTCCTTC
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TITLE JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 BB667509 LOCUS ACCESSION KEYWORDS VERSION DEFINITION Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japrel: 81-45-503-9222 Tagami,M., Tagawa,A., Takahashi,F., Muramatsu,M. and Hayashizaki,Y. MIKEN Mouse ESTs (Arakawa,T., et al Unpublished (2001)

Contact: Yoshihide Hayashizaki Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 728) BB667509 728 bp mRNA linear BB667509 RIKEN full-length enriched, adult male l musculus CDNA clone C730019M05 3', mRNA sequence. BB667509 Mus musculus BB667509.1 GI:16398958 house mouse. Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus. et al. Yokohama, Kanagawa 230-0045, Japan mRNA linear EST 24-OCT-: d, adult male liver tumor Mus 2001) EST 24-OCT-2001

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FEATURES
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Konno, H., Fukunishi Y., Shibata, K., Itoh, M., Carninci, P., Sugahar.
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URL:http://genome.gsc.riken.go.jp/
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Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
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Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
On Jul 10, 2000 this sequence version replaced gi:9008505.
Contact: Yoshihide Hayashizaki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 678)
                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB307800 RIKEN full-length enriched, adult male quadrigemina Mus musculus cDNA clone B230216H15 BB307800
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N
                                                                                  1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                             Fax: 81-45-503-9216
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    Hayatsu, N.,
  Sugahara, Y.,
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  Shibata, K.,
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AGCTTTCCACACAGAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACA 2113
                                                                                               CAAAGGCGACTATAATGCCTTGAGTGTCTGCCCCCAATATCATCTCATGAAGGACGCCAC 131
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Mapping of 1903 mouse cDNAs on mouse chromosomes. J. Struct. Punc. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Normalization and subtraction of capt-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
,S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
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1 162 c 163 g 177 t
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to Rot = 20.0 and
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/db_xref="taxon:10090"
/clone="B230216H15"
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/dev_stage="adult"
/lab_host="DH10B"
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Pred. No. 2.1e-116;
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Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

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agawa 230-0045, J agawa 230-0045, J ,Y., Shibata,K., ayashizaki,Y. ayashizaki,Y. ayashizaki of new hiscovery of new cawa,M., Ohara,E.	to 646) Carninci, P., Fukuda, S. Carninci, P., Fukuda, S. K., Hori, F., Ishii, Y., S., Matsuyama, T., Miyazz Okido, T., Saito, R., Sa a, K., Shinagawa, A., Shi Tagawa, A., Takahashi, F. I. and Hayashizaki Seris (Arakawa, T., et al [(2001)] Shihide Hayashizaki for Genome Exploration	646 bp mRNA linear EST 31-AUC IKEN full-length enriched, adult male corpora na Mus musculus cDNA clone B230216H15 5', mRNA seque GI:15402240		491 247 551	GCTGTGTGGAGGTAGTGCTATGTACAAACTTGCTTTAAAACTGGAGTTTGCAAAGTCAAC 371 CTGAGCATACACGCCTGAGGCTAGTCATTGGCTGGATTTATGAAGACAACACAGTTACAG 2353	AGCTTTCCACACAGAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACA 191  AGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGC 2173  AGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGC 251  AGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGC 251  CTTCCTACTCTCCCTTCCAGTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGGAGAG 2233  CTTCCTACTCTCCCTTCCAGTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGGAGAG 311  GCTGTGTGGAGGTAGTGCTATGTACAAACTTGCTTTAAAACTGGAGTTTTGCAAAGTCAAC 2293  [

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                         GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAAACAACATG
                                                                                                                ACAAGTGTGGCAGCAGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA 240
                                                                                                                                                                                                         ATGGTCCAACACACACCCCACGAGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAG 180
                                                                                                                                                                                                                                                                     GCCCTGCCTCGAGAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGG
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GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAAACAACATG
                                                                                    ACAAGTGTGGCAGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
                                                                                                                                                                             ATGGTCCAACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAG
                                                                                                                                                                                                                                                                                                                                                          GTGGCCAGTGGCCGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGC 148
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RIKEN integrated sequence analysis (RISA) system--384-format
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Y. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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/dev_stage="adult"
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99.8%;
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0; Mismatches 1
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126 CCAACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAGACAAG 189
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                                                                     GCCTCGAGAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGT 125
                                                                                                         CGGCGTCGGGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGCGCCCT 71
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Mammalla; Butheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 773)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMIII16 row: 1 column: 19
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High quality sequence stop: 768.
Location/Qualifiers
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                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5042466"
/clone="NGI_CGAP_Kid14"
/clone_1b="NCI_CGAP_Kid14"
/lab_host="UH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 194 c 204 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"/strain="FVB/N"
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                                                                                                                                                                                                Score 489.4; DB 1
Pred. No. 3.9e-89;
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musculus cDNA clone
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REFERENCE
AUTHORS
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasak. O., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)
                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                 Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RIKEN integrated sequence analysis (RISA)
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RIKEN full-length enriched, adult male l
cDNA clone C730019M05 5', mRNA sequence
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                                                                   384 multicapillary sequencer.
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                      Itoh, M.,
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                                                                                                                                                                                       GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATG
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TCCGGCGGCA----AATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCT
                                                  AATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCT
                                                                                                                                               GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAAACAACATG
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Conservative

<u>.</u>

Score 488.4; DB 1 Pred. No. 6.4e-89; D; Mismatches 1

DB 10; 1;

Length

4.

Gaps

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360

300

241

301

240

181 180 121 120 61 60 18.9%;

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2) . 281-289 (200 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp)
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further details
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     193
                                                                                                                                                                                       was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I pBluescript KS(+) after bulk excision from Lambda FLC I Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, where the state we gratefully acknowledge."

178 c 184 g 154 t 1 others
                                                                                                                                                                                                                                                                                                                              /note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
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lab_host="DH10B"
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                                                                                                 Local Similarity
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 430.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mq66h01.r1 Soares_thymus_2NbMT Mus_musculus_cDNA_clone_IMAGE:583729
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                                                                   Conservative
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:583729"
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|sex="male"
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                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                             Seq primer: -40UP from Gibco
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 431) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                      MGI:1453973
                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3811861"
                                                                           ocation/Qualifiers
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/dev stage="10 weeks"
/lab\_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site\_
/note="0: Sall; Cloned unidirectionally. Primer: "

Oligo dT.

clone\_lib="NCI\_CGAP\_Li10" /sex="female"

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JOURNAL COMMENT
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AUTHORS
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IMAGE Consortium (info@image.llnl.gov) for further information. MGI:694245
Seq primer: -28ml3 ravo pm f
                                                                                         Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Ld Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 425)
1 (bases 1 to 425)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Du
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Materston,R.
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lab_host="DH10B"
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|strain="C57BL/6J"
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                                        AAAAAAAAA 2581
                                                                                                                                                                                             CCCTGTCAGGCTGTCTGTCAGGTTGGGTCTGTCTTGCACTGCCCATGCTCTATGCTGCAC 2511
                                                                                                                                                                                                                                                                                AGCTGGGTAATGATTATCACTGAGAACCACGCACTCTGGCCATGAAGTAATACGGCACTT 245
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                                                                                                                                                                     CCCTGTCAGGCTGTCAGGTTGGGTCTGTCTTGCACTGCCCCATGCTCTATGCTGCAC
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1 (bases 1 to 370)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector to vector length is 377
Seq primer: -28ml3 rev1 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:973013"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
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Pred. No. 3.4e-64;
0; Mismatches 2
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CTTCTGAGATATGTTTCCATCACACGTCTGTCGCTTCACTGACTTTCTTCAAAACTACT CATCTGAAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAAACCATT 120

1710

AGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCCATTAAGGTTCTTGTGGTTTACC 60 AGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTGGTGGTTTATC 1650

1651

61

Query Match Best Local Similarity

14.1%; 76.0%;

Matches 465;

Conservative

0;

Score 366; DB 14; Pred. No. 4.2e-64; 0; Mismatches 145;

Length 652; Indels

2:

Gaps

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1591

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REFERENCE
AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97044477
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                       188
/db_xret="caxon: your closes" (71 phage resistant) (clone_lib="UI-E-DW1"
/clone_lib="UI-E-DW1"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant) "
/note="C0rgan: eye; Vector: DT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-E-DW1 is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into DT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tall. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                              AI616016 518 bp
mg66h01.y1 Soares_thymus_2NbMT Mus
5', mRNA sequence.
AI616016
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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EST.
                                                                                                                                                                                             correct orientation)
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                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 518)
                                                                                                                                                                             primer: -40RP from Gibco
                                                                                                                                                 quality sequence stop: 416.
Location/Qualifiers
                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                            /db xref="taxon:10090"
/clone="IMAGE:583729"
/clone=lib="Soares_thymus_
             /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
note="Vector: pT7T3D-Pac (Pharmacia) with a
                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA linear EST 21-APR-1999 musculus cDNA clone IMAGE:583729
                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
; Murinae; Mus
 modified
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Query Match
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                                                                                                                                                                                                                                                                                                                            prime, mF
AL565993
                                                                   Genoscope - Centre National de So
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verto Mammalia; Eutheria; Primates; Catarrhini; Hor 1 (bases 1 to 908)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                          AL565993.1
EST.
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prime, mRNA sequence.
                                                                                                                          Contact: Genoscope
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/db_xref="taxon:9606"
                                                  Location/Qualifiers
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Pred. No. 7.4e-63;
0; Mismatches 7;
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sapiens cDNA
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                                                                                                       Sequencage
                                                                     Web : www.genoscope.cns.fr.
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5', mRNA sequence

Bennett, G.A.,

CDNA

Smith, T.P.L.,

.P.L., Casas,E Laegreid,W.W.

Ë

Euteleostomi; Sus.

4SD

mRNA

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EST

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Query Match
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                                        TGAAGCCTTCCTACTCCCCTTCCAGTGACAATGCTGTGTGACGACTCTGAA
      TAAAGSCTYCCTATCCCMCCAATTACAGGGMAAAAACGTGTGATGATCCTGAA
                                                                                                                                   CACAAGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAA--TAGAGACTC 2167
                                                                                                                                                                                                             CCACAGCTTTCCACACAGAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCT
                                                                                                                                                                                                                                                                                              CCTCAAAGGCGACTATAATGCCCCTGAGTGTCTGCCCCCAATATCATCATCATGAAGGA-CG
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                                                                                         CACAASCCTGCCACGATGGCTGCTGCTTGTAGCCCMCCCATGAGAAGCAAGAGACYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CSODF016YG03"
/clone lib="LTI F1013"
/dev stage="pooled tissue from
week, 24 week and 26 week)"
/lab host="PH10B"
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Pred. No. 2.1e-62;
2; Mismatches 195;
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Matches 410
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AATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCT
                                                                                           GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACCATG
                                                                   GATGCCAGTATCCGATTGTTGAAGGCCACCAAGATCTGTGTGACGGGCAAGAGCCAGAAG
                                                                                                                                                                              ACAAGTGTGGCAGCAGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
                                                                                                                                                                                                                                                                     ATGGTCCAACACACACTCACTCCAGGAGAGTTGAGGGACCTCCAAGTGGAACTCGTCAAG
                                                                                                                                                                                                                                                                                                                                                        GCCCTGCCTCGAGAGCCGACTATTCAGTGTGGGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
                                                                                                                                                                                                                                          ATGGTTCGACACGCTCTGACCCCAGGAGACTTGAGGGACCTCCGAGTGGAACCTATTAAA
                                                                                                                                                                                                                                                                                                                               GCCATGCCTCCAGAGCCGACAATTCAGTGTGGCTCTGAGCCTGGACTGTCTCCAGAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                GCGGGAAGTCGCCCGCGATGTTACTAGTGCTGCTGAGCCTGGCCGCGCTGTGCTGGGGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGCCAGTGGCCGGGCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGC 60
                                                                                                                                                        AGCAGTGTTGCAGTGGAGGACTATTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410;
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BG384365.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 91 row: J column: 1
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Dases 1 to 551)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennel and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and -minmatch 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG384365 551 bp 303426 MARC 1PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site 1: NotI;
Library made from pooled tissue from day 1
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L. .551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Sus scrofa"
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Pred. No. 1.4e-61;
D; Mismatches 94;
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AUTHORS
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BB284760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGAACTTCACCTCACCAGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P, Nishiyama,Y, Westover,A., Itoh,M., Nagaoka,S., Sasa
Carninci,P, Nishiyama,Y, Westover,A., Itoh,M., Nagaoka,S., Sasa
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                                                                     ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                            trebhalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone A930106009 3', mRNA sequence.
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                                                                                                                                                                                                                                            High-efficiency full-length cDNA cloning. Methods Enzymol. 303
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                visit our web site (http://genome.rtc.riken.go.jp) for
                        /clone="A930106009"
/clone_lib="RIKEN full-length enriched,
tissue_type="retina"
                                                                                   db_xref="taxon:10090"
                                                                                                      organism="Mus musculus"
                                                                                                                                                              ocation/Qualifiers
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BI360842.1 EST.

GI:15056870

BI360842 588 bp mRNA 388904 MARC 2PIG Sus scrofa cDNA 5', mRNA BI360842

mRNA

sequence

linear

EST

01-AUG-2001

pig. Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;

Sus.

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                                      TGTAACATTTTAATCTGTTAATGAATAATCCGTTTGGGAAGCTCTCAAAAA 2573
                                                                                                                 TGTCTGTCAGGTTGGGTCTGTCTTGCACTGCCCATGCTCTATGCTGCACGTAGACCGTTT 2522
                                                                                                                                                                                                              ATTATCACTGAGAACCACGCACTCTGGCCATGAAGTAATACGGCACTTCCCTGTCAG-GC 2462
                                                                                                                                                                                                                                                                           ACAGTTACAAACAATAATGAGTGGGACCTACATTTGGGATATACCCAAAGCTGGGTAATT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T--GGGAGAGTCTGGTGGAGATAGGTGCTATGTACAAACTTGCTTTGAAACTGGATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTCTGAAGCCTTCCTACTCTCCCTTCCAGTGACAAATGCTGTGTGACGACTCTGAAATG 2223
                                                                                                                                                                                  ATTATCACTGAGAACCACGCACTCTGGCCATGAGGTAATACGGCACTTCCCTGTCAGTGC
                                                                                                                                                                                                                                                                                                                                                                    CANAGTCAACCGGAGCATACACGCCTGAGGCTAATCATTGGCTGGATTTATGAAGACAAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCTGAAACCTTCCTACTCTCCCGTCCAGTGACAGATGCTGT-TCACGACTCTAAATTT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACGGTCACAAGCCCCCCATGATAGCTGTTCACC--TGTTAGTCCAGCCGGGGGATAGAC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 27 Longwood Ave., Boston, MA02115, USA, whose assistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contributed to prepare
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 141 row: I column: 23
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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endometrium, hypothalamus, pituitary, and placenta."
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Search completed: May 28, 2003, 10:13:50 Job time: 3619.13 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-10-173-705-39	0-173-697-39	-10-173-695-39	-10-184-658-39	0-176-993-39	-10-176-992-39	-10-176-9	-10-176-987-39	-10-176-985-39	-176-750-39	-10-176-747-39	-10-176-492-39	-176-488-39	-10-175-743-39	-10-175-740-39	-10-175-739-39	74-588-39	-10-174-582-39	-10-174-579-39	-10-174-572-39	-10-173-700-39	80-557-39	-10-180-552-39	0-176-913-39	-10-176-757-39	82-39
equence 39	e 399,	equence 399,	equence 399,	е 399,	equence 399,	e 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	е 399,	equence 399,	equence 399,	e 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,	equence 399,

## ALIGNMENTS

RESULT 1

US-09-778-971-4
; Sequence 4, Application US/09778971
; Patent No. US20022012639A1
; Patent No. US20022012639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9 SEQ ID NO 4 LENGTH: 2589

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; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of mouse Evi27
US-09-778-971-4
                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2589;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2589; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                 1 GTGGCCAGTGGCCGGCCCATGTTGCTAGTGTTGCTGATCTTGGCTGCATCGTGCAGGAGC
                   ACAAGTGTGGCAGCAGAGGAGTTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGCA
                                                              ATGGTCCAACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAG
                                                                                ATGGTCCAACACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAG
                                                                                                                                 GCCCTGCCTCGAGAGCCGACTATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGG
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				TAAGTGTGTGTGTGTGTTTTGTGTGTGTGTGTGTGTGTG	CTTAAAGCITCCGIGGAAGAATGGITTCCTATTTAGATCTGTTGTCTCTCATATCTGAAG 1	TIGITITCCGIGICACCICCIGGAGACIGIITITGAIAAAGGIIGIACIIAAAGGAGAIIA 9	ACCACCTGGAGCTTCATGTCTGGAAGAGGCAGAACCTATATGTATTGTCAGCTCTCACTT	CCTATCTGGGCTGTGACATTGTTGTGAGGGTCGTGCCTACTAGGCATCTGGGTATCT	CCGGGGATATGAGGTTTGGGTATGAATCCCACAGAGGGCACTGAATTCTTCTCACTATGG 	GTCAAACTTACCTAGCTTGTTTCCATTCTGAAATTGTCTGATGCTTGCT	GGGCCAGAGGACTCAGTCATTCTGCCACCCCAGCCTCTGGCGTCGCTTTTTCATGACTTT 6	CCAGCAGCTAAACACCAGGCTCTCCGGATTTCAGCTCCTTTCCCATTACAATTTCCTCCT	GTGAACTTCACCTCGCCAGGGTGCACTCGTGAAAACACAGAAGTAACGTCCGGTGTATTT 	CTCATCAGCGCCCATAACATCCCCCAATGCTAATATGAATGA	TCCGGCGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTAT	AATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCAGACCT 3	GACGCCAGCATCCGCTTGTTGAAGGCCACCAAGATCTGCGTGAGTGGCAAAAACAACATG
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G 2460	1 ATGATTATCACTGAGAACCACGCACTCTGGCCATGAAGTAATACGGCACTTCCCTGTCA	40	Ş
A 24	. AACACAGTTACAGACAATAATGAGTGGGACCTACATTTGGGATATACCCAAAGCTGGGT 		P &
C 2340	GCATACACGCTGAGGCTAGTCATTGGCTGGATTTATGAAGA 	2 2	D Q
T 228	ANGTGTGGGAGAGGCTGTGTGGAGGTAGTGCTATGTACAAACTTGCTTTAAAACTGGAG 	2 2	dg Qy
222	AAGCCTTCCTACTCCCCTTCCAGTGACAAATGCTGTGTGACGACTG 	16	da Vo
A 216	1. AGAAACGCTCACAAGCCTGCCATGATAGCTGTTCACCCTTGTAGTCCACCCGGGG	10	B &
A 210	TGAAGGACGCCACAGCTTTCCACACAGAACTTCTCAAGGCTACGCAGAGCATGTC	04	D X
» »	1 GGGGAGCAGACCTCAAAGGCGACTATAATGCCCTGAGTGTCTGCCCCCAATATCATCA		д Б
•⊅	1 GGGGAGCAGACCTCAAAGGCGACTATAATGCCCTGAGTGTCTGCCCCCAATATCAT	9	Q
NG 1980	1 TCTTTTGTAGTGATTTCAGCAGCCAGACGCATCTGCACAAATACCTGGTGGTCTATCTT 	192 192	40 40
CC 1920 CC 1920	1 GCCACATGAGGCAGCGCCAGGGAGAACTCTCAGGATCTGTTCCCTCTTGCCTTTAACC 	186	8
3 186		ω (	Db .
G 1860	1 AGAAAAAAGTGGTCTTCCTTCCTGAGGGCTGACCCGACCCTTTGTGACAGGGC		Q B
3G 1800	1) AGAAAAAGAAAATCGCCGAGATGGGGCCGGTACAGTGGCTGACCACTCAGAAGCAAGC	7	Q
3C 1740    3C 1740	31 GTCGCTTCACTGACTTTCTTCAAAACTACTGCAGAAGTGAGGTCATCCTTGAAAAATGG 	168 168	da Võ
T 1680	I IGCCCTCATTAAGGTCCTGGIGGTTIAICCTTCTGAGATAIGTTTCCATCACACCGTC		B &
C 162	1 ACCTAACTTGGAGGCAAGGAAGGACGTCCTTTCCTATTTCCACCATG	· in	. Db
CC 1620	31 ACCTAACTTGGAGGCAAGGAAGGACGACGAAGACGTCCTTTCCTATTTCCACCATGCTC		γQ
T 156		ίπ	Db.
T 156	1 GCTGGCTGCCTCTTCCTGGTGCTGCTGGTGGCTGTGTGGGTGCTGGCAGCTGGG	ίπ	o,
AG 1500  - 	1 TGCTTTGCTCAGAGACAAGTGCTCCCATCCCTCCAGATGACAACAGAGGCATGCTGGGA 	144 144	84 85
[ ]   TG 1440	31 AGCTGACCCATAITIACATACCTGCGGCAATGACTGCATCCGACGCGAAGGGACAGTTG		95 5
138		, iu	o do

Db 2461 GCTGTCTGTCAGGTTGGGTCTGTTATAAT  Qy 2521 TTTGTAACATTTTAATCTGTTAATGAATA Db 2521 TTTGTAACATTTTAATCTGTTAATGAATA Dy 2581 AAAAAAAA 2589  RESULT 2 US-09-778-971-3 Sequence 3, Application US/09778971 Sequence 3, Application US/09778971 Fatent No. US20020102639A1 SEREAL INFORMATION: APPLICANT: Shaughnessy, John D. TITLE DF INVENTION: Evi27 Gene Seque FILE REFERENCE: D6138 CURRENT FILING DATE: 2001-02-04 FRIOR APPLICATION NUMBER: US 60/180, PRIOR APPLICATION NUMBER: US 60/180, PRIOR FILING DATE: 2000-02-04 VUMBER OF SEQ ID NOS: 9 SEQ ID NO 3 I LENGTH: 1963 TYPE: DNA ORGANISM: Unknown FATURE: NAME/KEY: Drim transcript OTHER INFORMATION: CDNA of mouse Ev US-09-778-971-3 OUCTY Match Matches 1474; CONSETVATIVE 0; MI SEQ ID NO 3 I TTCACCATTCCCAGGCTGCCTAAACCACGT OUCTY Match Matches 1474; CONSETVATIVE 0; MI SEQ ID NO 3 I TTCACCATTCCCAGGCTGCCCAGACATCACTGC OUTTY MATCH MATCHES 1474; CONSETVATIVE 0; MI SEQ ID NO 3 I TTGGGGTTTTCTAGAACCAATCCCCTTGGAAAACAC OUTTY GGAAGCCTGTGGGAACCATCACTGC OUTTY ACTTCACAACCAATCCCCTTGGAAAACAC OUTTY ACTTCACAACCAATCCCCTTGGAAAACAC OUTTY ACTTCACAACCAATCCCCTTGGAAAACAC OUTTY ACTGGGGTTTTCTAGAAGTGCTGGGACAATAA OUTTAGGGGTTTTCTAGAAGTGCTGCGTGGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCT OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTTCTAGAAGTGCAGGGACAGTTCA OUTTAGGGGTTTCTAGAAGTGCAGGGACAGTTCT OUTTAGGGGTTTTCTAGAAGTGCAGGAAGTTCA OUTTAGGGGTTTCTAGAAGAGGAAGTGCTGGGAAGTTCA OUTTAGGGGTTTTCTAGAAACAACAACAACAGGGAAGTTCA OUTTAGGGGTTTCTAGAAACAACAACAACAGAGGAAGTTCTA OUTTAGGGGTTTCTAGAAACAACAACAACAACAACAACAACAACAACAACAACA	용 성
GCTGTCTGTCAGGTTGGGTCTGTTTAATCTTTTAATCTGTTAAAAAAAA	90
GCTGTCTGTCAGTGTGTTTTTTCCACTGCCATGCTCTAGTCTAGTGTAGTGTAGTGTTTCCATGCCATGCTCTAGTGTAGTGTTTTTTTT	GCTGTGTGGGTGCTGGCAGCTGGGATCTACCTAACTTGGAGGCAAGGAAGG

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1926	867 CCCATGCTCTATGCTGCF	뮍
2552	493 CCCATGCTCTATGCTGC	δ
2492 1866	2433 ATGAAGTAATACGGCACTTCCCTGTCAGGCTGTCAGGTTGGGGTCTGTCT	9d Vy
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	1687 GCTAGTCATTGGCTGGATTTATGAAGACAACACAGTTACAGACAATAATGAGTGGGACCT	뮍
2372	2313 GCTAGTCATTGGCTGGATTTATGAAGACAACACAGTTACAGACAATAATGAGTGGGACCT	Ş
2312 1686	2253 ATGTACAAACTTGCTTTAAAACTGGAGTTTGCAAAGTCAACCTGAGCATACACGCCTGAG	용 성
1626	1567 GTGACAAATGCTGTGACGACTCTGAAATGTGTGGGAGGAGGCTGTGTGGAGGTAGTGCT	Дb
2252	2193 GTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGGAGAGGCTGTGTGGGAGGTAGTGCT	γQ
1566	1507 TCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGCCTTCCTACTCTCCCTTCCA	дb
2192	2133 TCACCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGCCTTCCTACTCTCCCTTCCA	γQ
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1386	1953 CTGCACAAATACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAAGGCGACTATAATGCC	용 왕
$\sim$		дb
1952		γQ
1266	1207 GTCCCGACCCTTTGTGACAGTGCCTGTGGCCACAATGAGGGCAGCGCCAGGGAGAACTCT	Db.
1892		γQ
1206	1147 CAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGGTCTTCCTTC	Дb
1832		Q Q
1146		90
1772	1713 AGAAGTGAGGTCATCCTTGAAAAATGGCAGAAAAAAGAAAATCGCCGAGATGGGGCCCGGTA	Ş
1086	1653 TOTGAGATATGTTTCCATCACACCGTCTGTCGCTTCACTGACTTTCTTCAAAACTACTGC 17	B 8
		D
	1593 ACGICCTTTCCTATTICCACCAIGCTCCTGCCCCTCATTAAGGICCTGGIGGTTTAICCT	. S

RESULT 3
US-09-863-818A-1
; Sequence 1, Application US/09863818A
; Publication No. US20030092881A1

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; NAME/KEY: CDS
; LOCATION: (4)..(1509)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (46)..()
; OTHER INFORMATION:
US-09-863-818A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gorman, Daniel M.
ITILS OF INVENTION: MAMMALIAN RECEPTOR PROTEINS, REIFILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 22
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
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Best Local Similarity
Matches 853; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1796
                   1761
                                                                                                      1009
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ATGGGGCCGGTACAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGGTCTTCCTT
                                              CAAAACTACTGCAGAAGTGAGGTCATCCTTGAAAAATGGCAGAAAAAGAAAATCGCCGAG
                                                                                                                   GTGGTTTATCCTTCTGAGATATGTTTCCATCACCACCGTCTGTCGCCTTCACTGACTTTCTT
                                                                                                                                                                          AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTG
                                                                                                                                                                                                                                                                                              TGCGGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTTGCTCAGAGACAAGTGCT 1463
                                                                                                                                                                                                                                                                                                                                                                                                              ATCCCGGTGACTGAGGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTACATACC 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGGGTTTTCTAGAGTGCTGG-----AGAATAAACTGATGAGGACGTCTGTAGCC 1343
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                                                                                                                                                          AGGATCAAGAAGACTTCCTTTTCTA---CCACCACACTACTGCCCCCCATTAAGGTTCTT 1008
                                                                                                                                                                                                                 TGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTC
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Pred. No. 6.6e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 252;
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; Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GÉNERAL INFORMATION:
APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and
; FILE REFERENCE: D6138
FILE REFERENCE: D6138
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; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA o:
US-09-778-971-1
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LENGTH: 1827
                                                                                                                                                                                                                                                                                    Matches 852;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/778,971
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/180,374
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                           1173
                                 1293
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RESULT 5
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Sequence 17, Application US/09886404
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                                  GENERAL INFORMATION:
APPLICANT: Medlock, Eugene
APPLICANT: Yeh, Richard
APPLICANT: Silbiger, Scott
APPLICANT: Elliot, Gary S.
              APPLICANT:
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Silbiger, Scott I
Silliot, Gary S.
Elliot, Gary S.
Nguyen, Hung Q.
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FILE REFERENCE: 01017/37128B
CURRENT APPLICATION NUMBER: US/09/886,404
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/810,384
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-66,159
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17
LENGTH: 1841
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US-09-886-404-17
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Matches 852; Conserv
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FEATURE:
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Pred. No. 2.2e-199;
D; Mismatches 253;
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CURRENT APPLICATION NUMBER: US/09/886,404
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/810,384
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR APPLICATION NUMBER: 60/213,125
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PALENTIN Ver: 2.0
SEQ ID NO 19
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; LOCATION: (50)..(1729)
US-09-886-404-19
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Best Local Similarity 75.9%;
Matches 852; Conservative
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APPLICANT: Wedlock, Eugene
APPLICANT: Yeh, Richard
APPLICANT: Silbiger, Scott
APPLICANT: Elliot, Gary S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09886404
Patent No. US20020037524A1
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo :
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Elliot, Gary S.
APPLICANT: Nguyen, Hung O.
APPLICANT: Jing, Shuqian
TITLE OF INVENTION: IL-17 Like Molecules and
FILE REFERENCE: 01017/37128B
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2015
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AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA
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Pred. No. 2.4e-199;
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                          TACTCTCCCTTCCAGTGACAAATGCTGTGACGACTCTGAA
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                                                        CACGATGGCTGCTGCTTGTAGCCCACCCATGAGAAGCAAGAGACCTTAAAAGGCTTCC
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US-09-863-818A-3
; Sequence 3, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:

Chen, Jian Filvaroff, Ellen

THEREOF

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RESULT 8

US-09-474-503-11

; Sequence 11, Application US/09874503

; Patent No. US20020177188A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
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Best Local Similarity
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TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
PRIOR FILING DATE: 2000-05-24
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NAME/KEY: CDS
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GENERAL INFORMATION:

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FILE REFERENCE: P138IR1C1P3(US)
CURRENT APPLICATION NUMBER: US/09/874,503
CURRENT APPLICATION NUMBER: US/09/874,503
CURRENT FILING DATE: 2001-06-05
PRIOR FILING DATE: 2000-11-28
PRIOR PPLICATION NUMBER: US 60/244,072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/213,807
PRIOR FILING DATE: 2000-06-22
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APPLICATION NUMBER: US
FILING DATE: 2000-12-01
APPLICATION NUMBER: US PCT/US00/30873
FILING DATE: 2000-11-10
APPLICATION NUMBER: US PCT/US00/23328
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 09/644,848
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                                                                                                                 FILING DATE:
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Goddard, Audr
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Hymowitz, Sarah G.
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; ORGANISM: Homo Sapien
US-09-874-503-11
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Best Local Similarity 77.1
Matches 805; Conservative
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LENGTH: 1515
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FILING DATE: 2000-03-21
APPLICATION NUMBER: US PCT/US00/05841
FILING DATE: 2000-03-02
APPLICATION NUMBER: US PCT/US00/05601
FILING DATE: 2000-03-01
FILING DATE: 2000-03-01
FILING DATE: US PCT/US00/04341
APPLICATION NUMBER: US PCT/US00/04341
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APPLICATION NUMBER: US
FILING DATE: 2000-06-02
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ATGGGGCCGGTACAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGGTCTTCCTT
                                    CAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAG
                                                          CAAAACTACTGCAGAAGTGAGGTCATCCTTGAAAAATGGCAGAAAAAGAAAAGAAAATCGCCGAG
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                                                                                                                                                                                                              AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTG 1640
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                                                                                                                                                                             AGGATCAAGAAGACTTCCTTTTCTA---CCACCACTACTGCCCCCCATTAAGGTTCTT
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77.1%;
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Pred. No. 1.1e-193;
0; Mismatches 224;
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APPLICANT: WOOD, MALTICE
APPLICANT: YASHURA, DANIE1
FILE REFERENCE: P1381R1C1P4 (US)
FILE REFERENCE: P1381R1C1P4 (US)
CURRENT APPLICATION UNMBER: US/10/000,157
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/13621
PRIOR APPLICATION NUMBER: 60/13023
PRIOR APPLICATION NUMBER: 60/13023
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/13023
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/134287
PRIOR APPLICATION NUMBER: 60/138387
PRIOR APPLICATION NUMBER: 60/172096
PRIOR APPLICATION NUMBER: 60/172096
PRIOR APPLICATION NUMBER: 60/17481
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APPLICANT: Filva
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Williams, P.Mickey
Wood, William
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VanLookeren, Menno
Vandlen, Richard
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Hillan, Kenneth
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Grimaldi, J.Christopher
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NUMBER OF SEQ
SEQ ID NO 11
LENGTH: 1515
TYPE: DNA
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RPPLICATION NUMBER: PCT/US00/30873
RPPLICATE: 2000-11-10
PTLING DATE: 2000-11-10
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FILING DATE: 2001-07-30
APPLICATION NUMBER: 09/929404
                                                                                 FILING DATE: 2001-0 APPLICATION NUMBER:
                                                                                                                                APPLICATION NUMBER: PCT. FILING DATE: 2001-06-20
                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/17800 FILING DATE: 2001-06-01
                                                                                                                                                                                                                                               FILING DATE: 2000-12-01
APPLICATION NUMBER: PCT/US00/34956
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APPLICATION NUMBER: PCT/US99/10733
FILING DATE: 1999-05-14
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FILING DATE: 2001-08-16
APPLICATION NUMBER: PCT/US99/05028
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APPLICATION NUMBER: 09/380142
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APPLICATION NUMBER: 09/311832
                                                                                                                  APPLICATION NUMBER: PCT/US01/21066
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FILING DATE: 2001-03-22
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NUMBER: PCT/US01/06520
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ORGANISM: Homo

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Pred. No. 1.1e-193;
0; Mismatches 224;
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US-10-063-547-157
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Best Local Similarity
Matches 805; Conserv
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 157
LENGTH: 1515
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APPLICANT: Eaton, Dan L.
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P93290R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
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APPLICANT:
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AGGATCAAGAAGACTTCCTTTTCTA----CCACCACACTACTGCCCCCCATTAAGGTTCTT 1011
                        AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATCCTCCTGCCCCTCATTAAGGTCCTG 1640
                                                           ---CTGCTGGTGGCTGTGTGGGTGCTGGCAGCTGGGATCTACCTAACTTGGAGGCAAGGA
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Grimaldi, Christopher J
Gurney, Austin L.
Watanabe, Colin K.
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Gerritsen, Mary E.
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Pred. No. 1.1e-19
0; Mismatches 22
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ches 224;
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APPLICANT: YANSURA, DANIEL
FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND
FILE REFERENCE: P1381R1C1P1 (US)
CURRENT APPLICATION UMMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR APPLICATION NUMBER: PCT/US90/04341
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
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US-09-747-259-11
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Williams, P.Mickey
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Vandlen, Richard
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; ORGANISM: Homo Sapien
US-09-747-259-11
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Best Local Similarity
Matches 805; Conserv
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APPLICATION NUMBER: US 60/242,837
FILING DATE: 2000-10-24
APPLICATION NUMBER: PCT/US00/30873
FILING DATE: 2000-11-10
APPLICATION NUMBER: US 60/253,646
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APPLICATION NUMBER: US
FILING DATE: 2000-06-22
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APPLICATION NUMBER: PCT/US00/23328
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              GTGGTTTATCCTTCTGAGATATGTTTCCATCACACCGTCTGTCGCTTCACTGACTTTCTT
                                                                                                                                            ---CTGCTGGTGGCTGTGTGGGTGCTGGCAGCTGGGATCTACCTAACTTGGAGGCAAGGA 1580
                                                                                                                                                                                                                                                                                                                ATCCCGGTGACTGAGGAGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTTACATACC 1403
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GTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
                                                                          AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTG 1640
                                                                                                                  TGCGGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGCT 1463
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Pred. No. 1.1
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                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo
US-10-174-590-399
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers Luc
APPLICANT: Goddard, Andrey
APPLICANT: Godowski, Paul
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CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrap)
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 399
LENGTH: 1515
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                              Matches
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACCOUNTY THE SAME
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Godowski, Paul
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Pred. No. 1.1e-193;
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RESULT 13
US-10-176-758-399
; Sequence 399, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Kevin P.
; APPLICANT: Chen, Jian
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APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Paulonghi: 1515
TYDE: DNA
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Best Local S
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ORGANISM: Homo Sapien
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                                                                           AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCCTCATTAAGGTCCTG 1640
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Pred. No. 1.1e-193;
0; Mismatches 224;
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; NUMBER OF SEQ ID
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo S
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US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
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                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                  Matches 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3233R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E APPLICANT: Gerritsen, M
                                                                                                                                                                                                                                                                                                                                                                                                                 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 170
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CURRENT FILING DATE: 2002-05-03
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                          TIGGGGITTITCTAGAGIGCIGG-----AGAATAAACIGAIGAGGACGICIGIAGCC 1342
                                                                                             AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292
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Filvaroff,Ellen
Gerritsen,Mary E.
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77.1%;
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APPLICANT: APPLICANT: APPLICANT:

Pan, James Smith, Victoria Watanabe, Colin I Wood, William I. Zhang, Zemin

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APPLICANT:

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US-10-175-737-399
; Sequence 399, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Panil J.
; APPLICANT: Godowski, Panil J.
; APPLICANT: Godowski, Panil J.
; APPLICANT: Godowski, Panil J.
; APPLICANT: Godowski, Panil J.
; APPLICANT: Pan, James
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; SEQ ID NO 399
; SEQ ID NO 399
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399
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Best Local Similarity 77.1
Matches 805; Conservative
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Search completed: May 28, Job time: 332.439 secs 2003, 10:38:02 밁

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Result
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2: /cgn2_6/ptodata/1/
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Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 1, Appli	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 13, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli

## ALIGNMENTS

RESULT 1 US-08-222-177A-24/c

SAME

DE: DI JRCE: HOMO JISOLI SE: BI JURCE: Ed40 GENOMI	REFERENCE/DOCKET NUMBER: 09 ; TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 831-2106 ; TELEFAX: (608) 831-2106 ; TELEFAX: (608) 831-2106 ; INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 259 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	COUNTRY: COUNTRY: COMPUTER READABLE FORM: REALIZE FORM: MEDIUM TYPE: Floppy di COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PATENTING SYSTEM: PC-D SOFTWARE: PATENTION NUMBER: US FILING DATE: CLASSIFICATION UNMER: US FILING DATE: CLASSIFICATION NUMBER: US FILING DATE: 21-APPLICATION NUMBER: US FILING DATE: 21-APPLICATION NUMBER: SETAL CHATLES S. REGISTRATION NUMBER: 3	Applicati 82979 82979 RMATION: Weber: NVENTION: NVENTION: SEQUENCES ENCE ADDR E: DeWit 8000 Exc adison Wisconsin
WA (genomic) sapiens ATE: Caucasian Lood	ET NUMBER: 09865.601  N INFORMATION:  8) 831-2100  ) 831-2106  ) B31-2106  2 ID NO: 24: EXISTICS: acid acid double	disk patik DOS/ eleas A: US/08 US/08 US/08	on US/08222177A  James L.  LENGTH POLYMORPHISMS IN  (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING :- 460 ESS:  t Ross & Stevens, S.C. elsior Drive, Suite 401

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Matches 55
                                                                         Sequence 14, Application Patent No. 5670367 GENERAL INFORMATION:
APPLICANT: DORNER, F.
                           APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Majndant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymorase Chain
CORRESPONDENCE
               NUMBER OF SEQUENCES:
                                             APPLICANT:
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TITLE:
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IDENTIFICATION METHOD: experime
OTHER INFORMATION: /evidence= E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Weber, J. L. AUTHORS: Kwitek, A. E. AUTHORS: May, A. E. TITLE: Dinucleotide repeat polymorphisms at the TITLE: D5S107, D5S108, D5S111, D5S117, and D5S1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /rpt_type= "tandem"
OTHER INFORMATION: /rpt_family= "(dC-dA)n.(dG-dT)n"
OTHER INFORMATION: /citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 388-396
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 4035-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL: Ni
VOLUME: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only one strand sequenced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1..259
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OTHER INFORMATION:
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LOCATION: 65..85
LDENTIFICATION METHOD:
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                                                                                                                                                                                                              GCTTTGGAA 157
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                                                                                                            4, Application US/08232463
5670367
                                                                                                                                                                                                                                                                                                                                                             Similarity
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/citation= ([1])
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/standard_name= "PCR primer"
/citation= ([1])
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/evidence= EXPERIMENTAL
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Pred. No. 0.00066;
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INFORMATION FOR SEQ ID NO:
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1380 YYYYYYYYYYYYYYYYYYYYYYY
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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CITY: Alexandria
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Local S.
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite
                          GAAATTGTCTGATGCTTGCTTC 711
                                                                                 CCAGCCTCTGGCGTCGCTTTTTCATGACTTTGTCAAACTTACCTAGCTTGTTTTCCATTCT 689
                                                                                                              TGAAAACACAGAAGTAACGTCCGGTGTATTTCCAGCAGCTAAACACCAGGCTCTCCGGAT 569
                                                                                                                                                                                                                              TAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACTTCACCTCGCCAGGGTGCACTCG 509
                                                                                                                                                                                                                                                                                                                                               TTCAGCTCCTTTCCCATTACAATTTCCTCCTGGGCCAGAGGACTCAGTCATTCTGCCACC 629
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20; Conservative 202;
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DEDNESS: single
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Pred. No. 0.01;
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US-07-805-123C-2/c

sequence 2, Application US/07805123C

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Best Local Similarity 59.8
Matches 75; Conservative
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                   quence 2, Application US/08033081B tent No. 5498521
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NFORMATION FOR SEQ ID NO:
                                               APPLICANT: Dryja, Thaddeus P. APPLICANT: Berson, Eliot L. TITLE OF INVENTION: DIAGNOSIS TITLE OF INVENTION: DEGENERATION DEGENERATION DEGENERATION DEGENERATION OF SEQUENCES: 25
                                                                                                                                                                                                                                                          1996 GAATTG 1991
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ATTOKNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/069003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 Model 50
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CURRENT APPLICATION DATA:
                              CORRESPONDENCE ADDRESS:
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ADDRESSEE: Fish & Richardson
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CLASSIFICATION:
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                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                          GCATCCTAATGTGGGGCAGAGTTCCTTGTTGGGAAGGAATGCAGAGGTGGTGGAAACCCA 1997
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SS: single
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                 Fish & Richardson
Franklin Street
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                                                                 DIAGNOSIS OF HEREDITARY RETINAL DEGENERATIVE DISEASES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08222177A
Patent No. 5582979
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH
TITLE OF INVENTION: (dC-dA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/03,08
FILING DATE: March 11, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/825,296
FILING DATE: January 23, 1992
APPLICATION NUMBER: 07/469,215
FILING DATE: January 24, 1990
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         ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                               1996 GAATTG 1991
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 502 or 55SX
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                         COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                STATE:
                                                                                                                                                               CITY: Madison
                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/069005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2 Model 50Z or 55
OPERATING SYSTEM: MS-DOS (Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATCCTAATGTGGGGCAGAGTTCCTTGTTGGGAAGGAATGCAGAGGTGGTGGAAAACCCA 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02110-2804
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                                                                                                                                            Wisconsin
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                                                                                                                                                                                 E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                        LENGTH POLYMORPHISMS IN (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/033,081B
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Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
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RESULT 7
US-07-890-609-3
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               Sequence 3, Application US/07890609C Patent No. 6001588
                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 22846
TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08469461B Patent No. 5981178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.7%;
Best Local Similarity 93.9%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tsui, Lap-Chee
APPLICANT: Rommins, Johanna M.
APPLICANT: Kerem, Bat-Sheva
TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and
TITLE OF INVENTION: Mutations at Various Positions of the Gene
FILE REFERENCE: 3477-61, 033477/139840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-198
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 811-2100
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/469,461B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEO ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                      7681
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                                                                                                                                                                                                                       IMMEDIATE SOURCE: CLONE: mfd2rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                      TGTATACATGTATGTATTCAGTCTTTACTGAAATTAAAAAATCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (608) 831-2106
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Pred. No. 0.0015;
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US-09-051-969A-5
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GENERAL INFORMATION:
                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,969A
FILING DATE: 1998-09-30
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLESHNER, RAZ E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0652.1690000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 22846
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NUMBER OF SEQ ID NOS: 33
SOPTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and TITLE OF INVENTION: Mutations at Various Positions of the Gene FILE REFERENCE: 3477-61, 03347/139840 CURRENT APPLICATION NUMBER: US/07/890,609C
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APPLICANT: Rommins, Johanna M.
APPLICANT: Kerem, Bat-Sheva
                                                                                                                                                         TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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CORRESPONDENCE ADDRESS:
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                                   MOLECULE TYPE: DNA
                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
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NAME/KEY: CDS
                                                             TOPOLOGY:
                                                                                                                     LENGTH:
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Similarity 69.2%;
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                                                                                                                   2529 base pairs
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NOE, WOLFGANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                        (genomic)
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US-09-051-969A-5
                                                                                                                                                   US-08-486-343A-3
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                                                                                                            Query Match
Best Local
                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 3, Application US/08486343A
1080 GGTTATACCCTTACTCAAATGTAACAACTTTCACATTCCACATTCCCAGGCTGCCTAAACC 1137
                                                                  1051 GTGTGTGTGTGTGTGT 1068
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OPPERMANN, HERMANN
                                            799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                  NAME: PITCHER, Edmund R
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1..2997
OTHER INFORMATION: /no:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: HOPKINTON
                                                                                                           Local
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                                         GTGTGTGTGTGTGTGT 646
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                                                                                                           Similarity
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                                                                                                                                                                                                                                                                      2997 base pairs
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                                                                                                                                                                                                                                                                                                              (617)-248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                     DNA
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                                                                                                                                                                                                                  (genomic)
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                                                                                                           1.6%;
                                                                                                                                                                /note= "MOP1 TERMINAL SEQUENCE"
                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/486,343A
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Pred. No. 0.04
0; Mismatches
                                                                                                           Score 41.2; DB Pred. No. 0.092;
                                                                                             Mismatches
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                                                                                                                      DB 3;
                                                                                              48;
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                                                                                                                      Length 2997;
                                                                                              Indels
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US-08-222-177A-169/c
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            Sequence 169, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMOR
TITLE OF INVENTION: (dC-dA)n.(dG-d'
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (508)-435-09
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  1080 GGTTATACCTTTACTCAAATGTAACAACTTTCATTCACATTCCCAGGCTGCCTAAACC 1137
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: 1..2997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2997 base pairs
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SEQUENCES:
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                                                                                                                                                                                                                                                                                                            1.6%;
              LENGTH POLYMORPHISMS IN (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
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460
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Pred. No. 0
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CORRESPONDENCE ADDRESS:

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RESULT 12
US-08-720-484A-1/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/341,562
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LENGTH: 50 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 3
CLASSIFICATION:
                               APPLICATION NUMBER: US/08/720,484A
                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                         STREET:
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ZIP: 53717-1914
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                                                                                                                                             94080
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South San Francisco
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                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: DeWitt Ross & Stevens, S
8000 Excelsior Drive, Suite
                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                    DeSauvage, Frederic
Rosenthal, Arnon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (608) 831-2106
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                                                                                                                                                                                                                        Genentech, Inc
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              30-Sep-1996
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Pred. No. 0.012;
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Best Local Similarity
Matches 59; Conserv
                                                                                         NAME: SVODULG, 29,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P105/
TELECOMMUNICATION INFORMATION:
TPT.EPHONE: 650/225-1489
                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027070
FILING DATE: 30-Sep-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 998
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 30-Sep
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
        LENGTH: 3854 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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IOPOLOGY:
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Syoboda, Craig G.
Syoboda, Craig G.
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Pred. No. 0.14;
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Query Match

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Score 40.8;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NUMBER OF SEQ ID NOS: 5; SEQ ID NO 1; LENGTH: 3854; TYPE: DNA; ORGANISM: Rattus No. 6
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Best Local Similarity
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                    COMPUTER: IBM Compatible
OPERATING SYSTEM; DOS
SOFTWARE: FASESEQ Version 2.0
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/916,043
APPLICATION NUMBER: US/08/916,043
FILING DATE: 21-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/398,239
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: US 08/720,484
EARLIER FILING DATE: 1996-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DeSauvage, Frederic
APPLICANT: Rosenthal, Arnon
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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1155 Avenue of the Americas
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Search completed: May 28, 2003, 10:25:59 Job time: 286.066 secs

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თ	644.8	24.9	1818	22	AAD12581	Human protein hav
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œ	643.2	24.8	1713	24	ABA03202	Human IL-17 recep
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AAT65675	ABL32143	ABK31490	ABL70463	ABN54635	AAZ35748	AAZ52037	AAA75763	AAZ35747	AAZ52036	AAA75762	AAF98686	AAS18129	ABQ58257	ABQ59113	AAZ08982	AAL05374	AAS29828	ABA18493	AAA95789 ·	AAD13444	ABL61567	AAS18127	AAZ35746	AAZ52035	AAA75761	AAF92136	AAS09514	AAS46124	812	AAZ52046	AAA75772	ABA03201	AAD28777	320	AAD28776
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/transl_except= "(pos:162..163, aa:Cys-Leu)"
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Mouse interleukin-17 receptor related protein (Evi27) encoding cDNA #2

AAD13446;

06-NOV-2001 (first entry)

AAD13446 standard; cDNA; 2589

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                                                                                                                                                                                                                                                                                                                                                                 chromosome 14. Evi27 is a common site of retrovital integration in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful as antisense molecules to inhibit Evi27 protein or for chromosomal mapping or mutational analysis of Evi27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of Evi27 at the RNA or protein level is used in the treatment of diseases such as cancer or autoimmune diseases.
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This sequence represents human cDNA encoding a secreted protein. The cinvention relates to sequences AAA87725-A87774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain annibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmne diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy, diabetes; atherosclerosis; Alzheimer's disease; neurodegeneratiye disorder; graft rejection; dementia; hyperlipidaemia;
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21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
                                                                                                                                                                                                                                                                                                                                          Sequence 1796 BP; 514 A; 439 C; 399
                                                                                                                                                                                                                                                                                                                                                                     endogenous receptor.
DCRS6 polypeptide.
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/product= "Human DCRS6"
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                                                                                                                                                                                                                                                                                                             supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease and Farkinson's disease and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10758. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
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TATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCTGAA 1612
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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biodiversity; gene therapy; nutrition; ss.
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DB; AAM24349.
ATCCCGGTGACTGAGGAGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTACATACC 1403
                                                                                                                                               AACTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATC
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12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0723232.
02-FEB-2001; 2001US-266159P.
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neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
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          Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21; Evi27; retroviral integration; chromosomal mapping; mutational analysis BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;
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                                                                                                                                                                                GGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTTGAAGTG 1232
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                                                     TTGGGGTTTTCTAGAGTGCTGG------AGAATAAACTGATGAGGACGTCTGTAGCC 1343
                                                                                                                        AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1293
                                                                                                                                                              GGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTG
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Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dystunction cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; autoimmune disorder; obesity; anorexia; cachexia; glomerulonephritis;
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GGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTG

TTCACATTCCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACTGAGGCG 1172

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Best Loc Matches Query Match

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al Similarity 75.9 852; Conservative

24.8%; 75.9%;

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Score 643.2; DB 24 Pred. No. 1.7e-181; 0; Mismatches 253;

Indels Length

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Sequence

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522 A; 455

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448

other;

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The invention relates to nucleic acid molecules encoding Interleukin 17 (II-17)-like polypeptides. II-17 DNA can be used to modulate the levels of II-17 protein in an animal. The II-17 protein is useful for treating CC preventing or ameliorating a disease, such as immune system dysfunction CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease); CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel CC disease, transplant rejection, graft vs. host disease); infections (HIV, CC (hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin CC (osteoporosis, Paget's disease, hypercalcaemia) twascular system (epilepsy CC atherosels, heart failure, angiogenesis); tumours, cancers (lymphoma CC atherosels, heart failure, angiogenesis); tumours, cancers (lymphoma CC inflammation. The present sequence is human Interleukin-17 receptor B-2 (III-1788-2) NA
                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding Interleukin 17 (IL-17) - like polypeptides useful in the treatment, prevention and diagnosi diseases e.g. cancer -
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                                                                                                                                                                                                                                                                                                  Disclosure; Page 230-232;
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16-MAR-2001;
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                                (IL-17RB-2) DNA.
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                                                                                                                               TGTGCAGAACTTCTCCATGTCAAGCAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGC
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                                                                                                                                                                                                The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. oczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischaemia), eye disorders, reproductive disorders, tumours and
                                                                              1113
                                                                                                                                                                                                                                                                                                                                                                         Three human nucleic acids encoding interleukin 17 (IL-17) receptor like polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections) -
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12-MAY-2000; 2000US-204208P
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02-FEB-2001; 2001US-266159P
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AAD28777;

AAD28777 RESULT 12

AAD28777 standard; DNA; 2015 BP.

Query Match Best Local Similarity

24.8%; 75.9%;

Score 643.2; DB 24 Pred. No. 1.8e-181;

Length

Sequence

2015 BP;

541 A; 499

C; 475 G;

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T; 0 other;

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(rheumatoid arthritis, osteoarthritis, inflammatory joint disease); autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft vs. host disease); infections (HIV, (hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, sepsis); neuronal dysfunction (Alzheimer's, parkinson's disease); lung (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin (psoriasis, ezzema, wound healing); kidney (glomerulonephritis); bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atheroscie, heart failure, angiogenesis); tumours, cancers (lymphoma leukaemia); reproductive (infertility, miscarriage, endometriosis), eye (blindness, retinal neuropathy) and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-2000;
02-FEB-2001;
16-MAR-2001;
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                                                                                                                                                                                                                                         The invention relates to nucleic acid molecules encoding Interleukin 17 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels of IL-17 protein in an animal. The IL-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 234-236; 242pp;
                                                                                                                                                                                                                                                                                                                                                             diseases e.g. cancer
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                                        The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. lischaemia), eye disorders, reproductive disorders, tumours and
                                                                                                                                                                                                                                        Three human nucleic acids encoding interleukin 17 (IL-17) receptor polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections) -
                                                                                                                                                                                                                                                                                                                                                               Jing
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                    WPI;
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12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0723232.
02-FEB-2001; 2001US-266159P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anoretic; nootropic; neuroprotective; antiathmatic; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
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DB; AAM47458.
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Query Match
Best Local Sim:
Matches 852;

Similarity

24.8%; 75.9%;

Conservative

0;

Score 643.2; DB 24 Pred. No. 1.8e-181; 0; Mismatches 253;

DB 24; Length

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Gaps

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                    CATGATAGCTGTTCACCCTTGTAGTCCACCCGGGGGAA--TAGAGACTCTGAAGCCTTCC
                                                                             CACACAGAACTTCTCAAGGCTACGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGC
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                                                         TGTGCAGAACTTCTCCATGTCAAGCAGCAGCAGGTCAGCAGGAAAAAGATCACAAGCCTGC
                                                                                                                   GATTACAATGCTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTC
                                                                                                                                             GACTATAATGCCCTGAGTGTCTGCCCCCAATATCATCATCATGAAGGACGCCACAGCTTTC
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                                                                                                                                                              Matches 852;
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                         1173
                                                                                                                                                                                                                                                           The present sequence encodes a human interleukin 17-receptor-like protein (IL17RLP) variant. The IL17RLP polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to cellular activation; haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis,
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                                                                                                                     1113 TTCACATTCCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCACTGAGGCG 1172
                                                                                                                                                                                                                      Sequence 1918 BP;
                                                                                                                                                                                                                                                                                                                                                                                                          Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system relative treating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-647065/62.
P-PSDB; AAB18754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular activation; haemostasis; angiogenesis; tumour metastasis; cellular migration; ovulation; neurogenesis; arthritis; autoimmune disorder; systemic lupus erythromatosus; ss.
                                                                                                                                                                                                                                                 arthritis and
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 237-239; 247pp; English.
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AATTICACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292
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                                              GGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTG
                                                                                                      TACTCTCCCTTCCAGTGACAAATGCTGTGTGACGACTCTGAA
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                                                                                                                                                              Conservative
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                                                            CACGATGGCTGCTGCTTGTAGCCCACCCATGAGAGCCAAGAGACCTTAAAGGCTTCC
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                                                                                                                                                                                        CC protein (IL-17RLP). IL-17RLP is a homologue of the IL-17 receptor and has CC a wide range of cytokine receptor-like activities. IL-17RLP or its CC agonists may be used to enhance host defenses against resistant chronic CC and acute infections, e.g. mycobacterial infections, via the attraction CC and acute infections of microbicidal leukocytes. It may also be used to increase T-cell proliferation by stimulating IL-2 biosynthesis, for the CC treatment of T-cell mediated autoimmune diseases and lymphocytic CC leukaemias. IL-17RLP may also be used to regulate hematopoiesis and to Ct treat sepsis. Extracellular IL-17RLP domains may be used as antagonists CC iIL-17RLP. TL-17RLP agonists and antagonists can also be used to modulate IL-6 expression, useful in treatment of cancers such as CC myclomas, plasmacytomas and hybridomas and Lennert's Lymphoma. The CR present cDNA sequence encodes human IL-17RLP. This cDNA sequence was C derived from sequencing the HAPOR40 cDNA clone (ATCC deposit
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16-SEP-1998;
16-MAR-1999;
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                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides encoding interleukin-17-like receptor useful for diagnosis and treatment of immune system-related e.g. sepsis and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor; resistant chronic infection, acute infection, mycobacterial infection T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia; T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma; IL-6 expression; myeloma; plasmacytoma; Lennert's Lymphoma; ILmunupprotective; cytostatic; hematopoietic; proliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 141-143; 147pp; English
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P-PSDB; AAY70595.
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98WO-US19121.
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Pred. No. is the number of results predicted by chance to have a

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## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AF208109	RESULT 1
1 (bases 1 to 2589) Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G. and Shaughnessy, J.D. Jr.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus.	•	AF208109.1 GI:9246430	AF208109	mRNA, complete cds.	Mus musculus IL-17 receptor homolog short isoform precursor (Evi27)	AF208109 2589 bp mRNA linear ROD 17-JUL-2000		

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and Shaughnessy,J.D. Jr.
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/product="IL-17 receptor homolog precursor"
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/protein_id="AAP86049.1"
/db_xref="GI:9246429"
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LPSDVPTLCDSACGHNEGSARENSQDLFPLAFNLFCSDFSSQTHLHKYLVVYLGGADL
     KGDYNALSVCPQYHLMKDATAFHTELLKATQSMSVKKRSQACHDSCSPL"
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            ACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCCTCATTAAGGTCCTGGTGGTTTATCCT
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RESULT 3
BC026546
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS

BC026546 BC026546.1 MGC.

GI:20071644

BC026546 2018 bp mRNA linear ROD Mus musculus, interleukin 17B receptor; clone MGC:35924 IMAGE:5042466, mRNA, complete cds.

07-AUG-2002

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Oy 1233 F Db 594 F	Qy 1173 c	Qy 1113 T	Query Match Best Local Matches 145	BASE COUNT				CDS		FEATURES source				COMMENT	REMARK	REFERENCE AUTHORS TITLE	SOURCE ORGANISM
AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292 	GGAAGCCTGTGGGACCCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTTGAAGTG 1232	TAAACCACGTAATGAAATATAAAAAGCAGTGCACTGAGGCG 1172 	<pre>Match 56.0%; Score 1449.8; DB 10; Length 2018; Local Similarity 99.5%; Pred. No. 0; les 1454; Conservative 0; Mismatches 7; Indels 0; Gaps 0;</pre>	LESULETICOSACEINEGSARENSODIE PLAFNIEGESSQTHIHKYLVYLGGADL KGDYNALSVCPQYHLMKDATAFHTELLKATQSMSVKKRSQACHDSCSPL"  535 a 504 c 501 g 478 t	GCLMHWKYKKQCTEAGSLMDDJTACKKKEKMUEVNETURLGKEYTILLQCEDTURG GCLMHWKYKKQCTEAGSLMDDJTACKKKEKMUEVNETURDLGKEYTILLQCEDTURG FSRVLENKLMRTSVAIPVTEESEGAVVQLTPYLHTCGNDCIREEGTVVLCSETSAPIP PDDNRRMLGGMLPLFLVLLVAVMYLAAGTYLTMRQGRSTKTSFPISTMLLPLIKYLVV	/db xref="Locusid:50905" /db xref="Locusid:50905" /translation="MLLVLLILAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD /translation="MLLVLLILAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVELVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVELVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD LRDLQVETSVAAEEFSILMNISWILAAASCRSALPREPTIQCGSETGPSPEWMVQHTLTPGD	/codon_start=1 /product="interleukin 17B receptor" /protein id="AAH26546.1" /protein id="AAH26546.1"		/db_xref="taxon:10090" /map="FVB/N" /clone="MGC:35924 IMAGE:5042466" /tissue type="Kidney, normal. 5 month old male mouse."	passed the following selection criteria: matched mRNA gi: information/Qualifiers 1. 2018 /organism="Mus musculus"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 58 Row: m Column: 5 This clone was selected for full length semiencing because it	Contact: (Dickson, Mark) modepaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	ממבט	MGC help desk gapbs-r@mail.nih.gov rocurement: Jeffrey E. Green, M.D.	Gene Collection (MGC), Cancer Genemics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project IRL: http://mgc.nci.nih.gov	nammaria; burneria; kowemicia; sciurognachi; muridae; muridae; mus.  1 (bases 1 to 2018) Strausberg,R. Strausberg,R. Direct Submission Gubmisted (02-100-2008) Notional Institutos of Woolth Mammaliae	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-AUG-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Gand-Pierre,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-25A7
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                  Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L13729
Center clone name: 25_A_7
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Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105150 105249: gap of 100 bp in length 105250 106522: contrig of 1273 bp in length 106523 106622: gap of 100 bp in length 106623 108946: contrig of 2324 bp in length 108947 109046: gap of 100 bp 109046: gap of 1712 bp in length 109047 110758: contrig of 1712 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150407 150506: gap of 100 bp 150507 233879: contig of 83373 bp in length 23380 233979: gap of 100 bp
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137591 137690: gap of 100 bp
137691 150406: contig of 12716 bp in length
150407 150506: gap of
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Consensus quality: 230172 bases at l
Consensus quality: 231921 bases at l
Insert size: 210000; agarcse-fp
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847 2105: contig of 1259 bp in length

2106 2205: gap of 100 bp

2206 3019: contig of 814 bp in length

3020 3119: gap of 100 bp

3120 105149: contig of 100 bp

105149: contig of 100 bp
                                       /note="assembly_fragment"
137691. .150406
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129490. .137590
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121427. .129389
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110859. .113410
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109047. .110758
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105250. .106522
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                      AATGATTATCACTGAGAACCACGCACTCTGGCCATGAAGTAATACGGCACTTCCCCTGTCA
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                                                             ATCCCGGTGACTGAGGAGAGTGAAGGTGCGGTGGTTCAGCTGACCCCATATTTACATACC 1403
                                                                                                               TTGGGGTTTTCTAGAGTGCTGG------AGAATAAACTGATGAGGACGTCTGTAGCC 1343
                                                                                                                                                                        AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292
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                                                                                            Sequence
AX061651
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VVYPSBICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVV
FLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFREI
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/protein id="CAC25011.1"
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                     Gorman, D.M.

Mammalian receptor proteins; related reagents

Patent: WO 0190358-A 1 29-NOV-2001;

SCHERING CORPORATION (US)
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GCLDHIMKYKKCVKAGSLWDPNITACKKNEETVEVNFTTPLGNRYMALIQHSTIIG
FSQVEEPHQKKQTRASVVIPVTGDSEGATVQLTFYFFTCSDCIHKKGTVLCPQTGV
FFDLDNNKSKPGGMLPLLLLSLLVATWLVAGJYLWRHHERIKKTSFTTTLLPPIKV
PFPLLNMKSKPGGMLPLLLLSLLVATWLVAGJYLWRHHERIKKTSFTTTLLPPIKV
LVVYPSEICFHTICYFTEFLQNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKTVVVYFRE
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Sequence 56
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AX191534.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1818)
                                                                                                                                                                                                                                                                                                                                                                       Human proteins having hydrophobic domains
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                                                                                                                                                                                                                                                                                                                                              Patent: WO 0149728-A 56 12-JUL-2001;
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                           Conservative
                                                                                      /proteIn_id="CAC51160.1"
//db xref="G1:15209722"
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/translation="MSLVLSLLSALCRSATRICVTYFIGAHNIPNANMNEDGPSMSVNFTSP
GCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTFLGNRYMALIQHSTIIG
FSQVEEPHQKKQTRASVVIPVGDSEGAFVQLTPYFPTCGSDCIHKGTTVLCPQTGV
PFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKV
PFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKV
LVVYPSEICFHHTICYETEFLQNHCRSEVILEKWQKKKLAEMGPVQWLATQCKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKVVVVYFRE
IDTKNDVNALSVCRYNILMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
22 a 447 c 404 g 445 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: n Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9246432.
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Sequencing Center
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Villalon, D.K., Luna, R.A., Hale, S.M., H
A.M., Holloway, M., Telford, B, Hodgson,
Muzny,D.M., Gibbs,R.A.
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2042)
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     TATCCCACCAATTACAGGGAAAAAACGTGTGATGATCCTGAA
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                                                                            CCCATCCCTCCAGATGACAACAGACGCATGCCTGGGAGGCTGGCCTCTCTTCCTGGTG
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Patent: WO 0168705-A 6 20-SEP-2001;
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//tanslation="mmtrsy1Gppvelntvyr1Gahn1pnannnedgpsmsvnftspg
CLDHIMXXKKCVKAGSLMDPNITACKKNEETVEVNFTTTPLANRYMALIQHSTI1GF
SQVFEBHQKKQTRASVV1FVTGDSSGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVP
FPLDNNKSKPGGMLPLLLLSLLVATWVLVAGIYLMMRHERIKTSFSTTTLLPPIKVL
VVYPSEICFHTTICYFTSFLQNHCRSWILEKWQKKKIABMGVVGKAADKVV
FLLSNDVNSALSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFREI
DTXDDYNALSVCDKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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Submitted (24-NOV-1999) Myeloma and Transplantation Center, University of Arkansas for Medical Sciences, Markham St. Little Rock, AR 72212, USA Location/Qualifiers
                                                             2 (bases 1 to 1828)
Shaughnessy, J.D. Jr.
Direct Submission
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AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292
                                                                                                          GGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTTGAAGTG 1232
                                                                 GGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTG
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/protein id="AF86051.1"
/db_xref="G1:9246433"
/db_xref="G1:9246433"
/translation="MSIVLISLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
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ESQVFEPHQKKQTRASVVIPVTGDSEGATVQLIPYFPTCGSDCIRHKGTVVLCPQTGV
PFPLDNNKSKPGGWLPLLLGLLVATWVLVAGIYLMWRHERLKKTSFSTTTLLPPKV
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594. .596
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1781. .1786
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1299. .1301
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882. .995
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471. .476
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45. .1511
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VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFFLAFNLFCSDLRSQIHLHKYVVVYFRE
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1643. .1649
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312. .314
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db_xref="taxon:9606"
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RESULT 11
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AX253204 1841 bp Sequence 1 from Patent WO0168705 AX253204

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PAT 05-OCT-2001

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G	AGAACTTCTCAAGGCT) [	AGAACTCTCAAGACCTC		IGCTGGTGGCTGTGGG	GETTTTCTAGAGTGCTG
ACCITATICANCACAGE  ACCITATGAGGACGICTE  ACCITATGAGGACGICTE  ACCITATGAGGACGICT  CONTROL	ACGCAGAGCATGTCAGT	TRCCCCCTTGCCTTTAA  FACCTGGTGGTCTATCT                           FACCTGGTGGTGTCTACTT  FACCTGGTGGTGTCTACTT  FACCTGGTGGTGTCACTT	STCATCCTTGAAAAATT	GTGCTGCAGCTGGGAT	GAGAATAN GAGCCACACCAGAAGAN GAAGGTGCCACCAGAAGAN GAAGGTGCTACGGTGCN GAAGGTGCTACGGTTGT CATAAAGGAACAGTTGT AGACGCATGCTGGGAGGAACAGTTGT
1	GAAGAAACGCTCACAAGCCT AGGAAAAAGATCACAAGCCTT TAGAAGACTCTGAAGCCTT GCAAGAGACCTTAAAGGCTT GCAAGAGACCCTTAAAGGCTT TGAA 2220	TGGGGGAGCTGATCTAAGA TGGGGGAGCTGAAAGAGA TAGAGAGTTGATAGAAAAGAA TAGAGAGATTGATACAAAAGAA TAGAAGAGACGCACAGCTTTG TAGAAGGACGCCACAGCTTTG TAGAAGGATGCCACAGCTTTG	SICHGANAAGANAATCGCC	CTACCTAACTTGGAGGCAA	ACTGATGAGGACGTCTGTAGG

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                    AGGAGCACGAAGACGTCCTTTCCTATTTCCACCATGCTCCTGCCCCTCATTAAGGTCCTG
                                                                                   ---CTGCTGGTGGCTGTGTGGGTGCTGGCAGCTGGGATCTACCTAACTTGGAGGCAAGGA
                                                                                                                             TGCGGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                    AACTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATC
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                                                                                                                                                                                                                                                                                                                                  Jing,
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1 (bases 1 to 1841)
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// db xref="G1:15986347"

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/ tranalation="MSLVLUSLAALCRSAVPREPTVOCGSETGPSPEMMLQHDLIPGD
IRDLRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRC
NYTEAPQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPANNMEDGPSMSVNFTSP
GCLDHIMKYKKKCVKAGSLMDPNITACKKNEETVEVNFTTPLGNRYMALIQHSTIG
ESQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTGGSDCIRHKGTVVLCQTGV
FPPLDNNKSKPGGMLPLLLLSILLVATWVLVAGIYLMWRHERIKGTSFSTTTLLPPIKV
LVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKLAEMGPVQWLATQKKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFRE
IDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
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0; Mismatches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
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                       TTGGGGTTTTCTAGAGTGCTGG------AGAATAAACTGATGAGGACGTCTGTAGCC 1343
                                                                                     AATTTCACAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACGGGACACGACA 1292
 GGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTG
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Patent: WO 0168705-A 4 20-SEP-2001;
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LRDLRVEPVTTSVATGDYSILMNVSWYLRADASIRLLKATKICVTGKSNFGSYSCVRL
ECSGAIMARCDLNILGSSDRSASASRAAGTAGVGHQTWLIFVVPVEGGFTVLLVLNSS
AQAICLPRLPKYLGLQMTFSYIGFPVELNTVYFIGAHNIPOARMNEDGPSMSVNFTSP
GCLDHIMKYKKKCVKAGSLMDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTIIG
FSQVFEPHQKKQTRASVVIPVTGGSEATVQLTPYFPTGGNSTHKGTVVLCPQTGV
PFPLDNNKKSRGGMLPLLLSLLVATWVLVAGILYMMRHERIKTSPSTTTLLPPIKV
LVVYPSSICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQMLATQKKAADKV
VPLLSNDVNSYCDGTTGKSEGSPSENSQDLFPLAFNLFCSDLRSQHHLHKYVVVYFRE
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Sequence 19
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     human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                      GTGGTTTACCCATCTGAAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTT
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Il-17 molecules and uses thereof
Patent: WO 0208285-A 19 31-JAN-2002;
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//bb_xref="GI:18697006"
//bb_xref="GI:18697006"
//translation="MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGD
//translation="MSLVLLSLAALCRSAVGHQTWLIFVVFVEGGFTVLLVLNSS
AQAICLPRLPKVLGLQWTFSYIGFPVELNTVYFIGAHNIFNADKGDESNSVNFTSP
GCLDHIMKYKKKCVKAGSLWDPNITACKKNETVEVNFTTTPLGNRYMALIQHSTIIG
FSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCTRHKGTVVLCPOTGV
PFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKV
LVVVPSEICHHTICYFTEFLQNHCRABVILEKWQKKKLAEMGFVQWLATOKKAADKV
VFLLSNDVNSVCDGTCGKSEGGPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFRE
IDTKDDYNALSVCPKYHLMKDATAFCLELLHVKQQVSAGKRSQACHDGCCSL"
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/db_xref="taxon:9606"
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Pred. No.·1.3e-191;
0; Mismatches 253;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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LRDLRVEPVTTSVATGDXSILMRVSWVLRADASTRLKATKICVTGKSNFQSYSCVRC
NYTEAFOTOTRESGKWFTSYLGFPVELLWTVE IGAHNIPNANWEDGPSWSVGTVRC
NYTEAFOTOTRESGKWFTSYLGFPVELLWTVE IGAHNIPNANWEDGPSWSVNETSE
GCLDHIMKYKKCVKAGSLMDPNITACKKWEETVEVNFTTTPLGNRYMALIQHSTIIG
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PFPLDNNKSKFQGMLPLLLSLLVATWYLVAGIYLMRHERIKKTSFSTTLLPFIKV
LVVYPSEICFHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKV
VFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLHKYVVVYFRE
LDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL"
397 c 377 g 382 t
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/product="putative cytokine receptor
/protein_id="AK37428.1"
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